

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2005, 11:36:08 ; Search time 19.1667 Seconds
(without alignments)
25.100 Million cell updates/sec

Title: US-09-473-619D-1

Perfect score: 27

Sequence: 1 GDEVD 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	16	2 PL0137	protein kinase, 80
2	27	100.0	44	2 B43714	hydroxymethylgluta
3	27	100.0	133	2 E89817	hypothetical prote
4	27	100.0	134	2 A55580	dihydrodipicolinat
5	27	100.0	135	1 R3HS13	ribosomal protein
6	27	100.0	151	2 S37812	hypothetical prote
7	27	100.0	154	2 C70318	hypothetical prote
8	27	100.0	156	1 R3HS11	ribosomal protein
9	27	100.0	199	2 S17777	strG protein - Str
10	27	100.0	228	2 T04945	hypothetical prote
11	27	100.0	233	1 F69078	probable formate a
12	27	100.0	237	2 T46121	hypothetical prote
13	27	100.0	257	2 T25387	hypothetical prote
14	27	100.0	267	2 A69319	thiamin biosynthes
15	27	100.0	268	2 H83051	dihydrodipicolinat
16	27	100.0	343	2 B86468	probable DNA polym
17	27	100.0	349	2 AB1715	oxidoreductase hom
18	27	100.0	349	2 AG1341	oxidoreductase hom
19	27	100.0	352	2 E70249	hypothetical prote
20	27	100.0	355	2 C95843	probable DNA ligas
21	27	100.0	359	2 T16350	hypothetical prote
22	27	100.0	371	2 H97073	similar to toxic a
23	27	100.0	376	2 S76145	hypothetical prote
24	27	100.0	382	2 AG3161	conserved hypothet
25	27	100.0	385	2 JC2256	aspartate transami
26	27	100.0	385	2 G72659	probable type II D
27	27	100.0	387	2 H69080	aspartate transami
28	27	100.0	393	2 T05532	hypothetical prote
29	27	100.0	411	2 F90215	hypothetical prote

30	27	100.0	413	2 T07110	vacuolar proton-AT
31	27	100.0	413	2 J80142	glutamate synthase
32	27	100.0	420	2 H84182	hypothetical prote
33	27	100.0	423	2 E84027	molybdopterin bios
34	27	100.0	425	2 T41172	hypothetical prote
35	27	100.0	428	2 A44756	hydroxymethylgluta
36	27	100.0	436	2 G69466	3-hydroxy-3-methyl
37	27	100.0	440	2 A95564	unknown protein, 2
38	27	100.0	453	2 A96888	hypothetical prote
39	27	100.0	455	2 H69230	NADP-dependent gly
40	27	100.0	463	2 T39621	peptidyl prollyl ci
41	27	100.0	485	2 S26575	hemolysin - Aeromo
42	27	100.0	486	2 A25976	aerolysin precurs
43	27	100.0	486	2 T47647	hypothetical prote
44	27	100.0	488	2 S26576	hemolysin - Aeromo
45	27	100.0	489	2 I39672	hemolysin 2 - Aero

ALIGNMENTS

RESULT 1

PL0137

protein kinase, 80K - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 18-Jun-1993

C;Accession: PL0137

R;Deichert, U.; Weber, M.; Weber-Schaeuffelen, M.; Wollny, E.

J. Neurochem. 53, 1268-1275, 1989

A;Title: Isolation and partial characterization of an 80,000-dalton protein kinase from t

A;Reference number: PL0137; MUID:89361455; PMID:2769266

A;Accession: PL0137

A;Molecule type: protein

A;Residues: 1-16 <DEC>

A;Cross-references: UNIPARC:UPI0000177D3E

C;Comment: This protein has a novel serine/threonine-specific protein kinase activity.

Query Match 100.0%; Score 27; DB 2; Length 16;

Best Local Similarity 100.0%; Pred. No. 10;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5

DB 1 GDEVD 5

RESULT 2

B43714

hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) - Pseudomonas sp. (fragment)

C;Species: Pseudomonas sp.

C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 26-May-2000

C;Accession: B43714

R;Anderson, D.H.; Rodwell, V.W.

J. Bacteriol. 171, 6468-6472, 1989

A;Title: Nucleotide sequence and expression in Escherichia coli of the 3-hydroxy-3-methyl

A;Reference number: A43714; MUID:90078086; PMID:2687236

A;Accession: B43714

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-44 <AND>

A;Cross-references: UNIPARC:UPI00000BD792; GB:M31807; NID:G151370; PIDN:AAA25894.1; PID:

C;Superfamily: Methanococcus jannaschii hydroxymethylglutaryl-CoA reductase (NADPH)

C;Keywords: coenzyme A; oxidoreductase

Query Match 100.0%; Score 27; DB 2; Length 44;

Best Local Similarity 100.0%; Pred. No. 29;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5

DB 13 GDEVD 17

;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 189
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: Artificial
;; FEATURE:
;; OTHER INFORMATION: Synthetic peptide substrate
;; NAME/KEY: misc feature
;; OTHER INFORMATION: Artificial/Unknown = central protease recognition domain
US-09-394-019C-789

Query Match 100.0%; Score 27; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
DB 1 GDEVD 5

RESULT 6
US-08-665-643A-3
;; Sequence 3, Application US/08665643A
;; Patent No. 6288037
;; GENERAL INFORMATION:
;; APPLICANT: Talanian, Robert V.
;; APPLICANT: Ghayur, Tariq
;; APPLICANT: Hodges, John C.
;; TITLE OF INVENTION: SUBSTRATES AND INHIBITORS FOR CYSTEINE PROTEASE ICH-1
;; FILE REFERENCE: BBI-049CPCPA
;; CURRENT APPLICATION NUMBER: US/08/665,643A
;; PRIOR FILING DATE: 1996-06-18
;; PRIOR APPLICATION NUMBER: 08/592,943
;; PRIOR FILING DATE: 1996-01-29
;; NUMBER OF SEQ ID NOS: 89
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 3
;; LENGTH: 12
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: synthetic
;; OTHER INFORMATION: construct
;; OTHER INFORMATION: amino-terminal acetyl modification;
;; OTHER INFORMATION: carboxy-terminal amide modification
US-08-665-643A-3

Query Match 100.0%; Score 27; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
DB 2 GDEVD 8

RESULT 7
US-09-522-666-11
;; Sequence 11, Application US/09522666
;; Patent No. 6333167
;; GENERAL INFORMATION:
;; APPLICANT: Shuey, David
;; APPLICANT: Quiney, Elaine
;; TITLE OF INVENTION: Methods and Reagents for Identifying Inhibitors of
;; FILE REFERENCE: 6-00
;; CURRENT APPLICATION NUMBER: US/09/522,666
;; PRIOR FILING DATE: 2000-03-10
;; NUMBER OF SEQ ID NOS: 32
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 11
;; LENGTH: 12

;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: sequence
;; OTHER INFORMATION: encoding g-s-g linkers and caspase-3 cleavage
;; OTHER INFORMATION: sites
US-09-522-666-11

Query Match 100.0%; Score 27; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
DB 7 GDEVD 11

RESULT 8
US-08-789-738B-60
;; Sequence 60, Application US/08789738B
;; Patent No. 6455247
;; GENERAL INFORMATION:
;; APPLICANT: No. 6153380an, Garry P
;; APPLICANT: Rothenberg, S. M.
;; TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR
;; TITLE OF INVENTION: RECEPTOR PEPTIDES AND RNA MOLECULES
;; FILE REFERENCE: A6426110BRMSDSS
;; CURRENT APPLICATION NUMBER: US/08/789,331F
;; PRIOR FILING DATE: 1997-01-23
;; PRIOR APPLICATION NUMBER: 08/589,108
;; PRIOR FILING DATE: 1996-01-23
;; PRIOR APPLICATION NUMBER: 08/589,911
;; PRIOR FILING DATE: 1996-01-23
;; NUMBER OF SEQ ID NOS: 102
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 60
;; LENGTH: 15
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: anti-apoptosis
;; OTHER INFORMATION: sequence
US-08-789-738B-60

Query Match 100.0%; Score 27; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
DB 6 GDEVD 10

RESULT 9
US-08-789-738B-60
;; Sequence 60, Application US/08789738B
;; Patent No. 6455247
;; GENERAL INFORMATION:
;; APPLICANT: No. 6455247an, Garry P
;; APPLICANT: Rothenberg, Michael S.
;; TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT RECEPTOR
;; TITLE OF INVENTION: PEPTIDES AND RNA MOLECULES
;; FILE REFERENCE: A-64259-1
;; CURRENT APPLICATION NUMBER: US/08/787,738B
;; PRIOR FILING DATE: 1996-01-23
;; PRIOR APPLICATION NUMBER: 08/589,108
;; PRIOR FILING DATE: 1996-01-23
;; PRIOR APPLICATION NUMBER: 08/589,911
;; NUMBER OF SEQ ID NOS: 97
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 60
;; LENGTH: 15

002:2002US-0398143P.

0021 2002US-0402458P.

002; 2002US-0403289P.

002; 2002US-0406472P.

• THE 86040-207007: 1700

INCYTE CORP.

Swarnakar A. Griffin JA, Lee EA, Sprague WW;

AJA, Lee SY, Kable AE, Ison CH, Khare R, Chawla NK;

Jip, Jiang X, Jackson AA, Becha SD, Emerling BM, Jin P;

D7 Richardson TW, Yang J, Baughn MR, Gandhi AR, Nguyen

J, Kallick DA, Kearney L, Lu DAM, Gletzen K, Tribouley CM;

Blake JJ, Lu Y, Arvizu S;

4-122392/12

4-123321
ADT72043

in protein modification and maintenance molecules (PMMs), useful in diagnosing, treating and preventing diseases or conditions associated with aberrant PMM expression e.g. cancer, AIDS, epilepsy, or other diseases.

SEQ. ID NO 41: 387bp: English:

mentation relates to novel protein modification and maintenance of PMM. The polynucleotides which identify and encode PMM. The may be useful for the development of compositions with a protective, anticonvulsant, nontoxic, antihypertensive, antidiabetic, cerebroprotective, vasotropic, anti-HIV, antiallergic, antibacterial, antiinflammatory, endocrine-gen or thyromimetic activity. The polynucleotides are useful in diagnosing, treating, preventing diseases or conditions associated with the decreased expression of PMM, such as cell proliferative (for example, cancer, atherosclerosis), neurological (for example, epilepsy, stroke), immune/inflammatory (for example, AIDS, HIV), and developmental (for example, Hypothyroidism, Cushing's syndrome), disorders, or infections. These are also useful in assessing the effects of exogenous compounds on the expression of nucleic acid and protein sequences of PMM. The present sequence is that of a human PMM.

379 AA:

82.9% Score 34: DB 8: Length 379:

Similarity 71.4%; Pred. No. 8.3e+02;

5; Conservative 1; Mismatches 1; Indels 0; Gaps

CKGDEV D 7

CRGDETD 309

RESULT 8

AAR66771

ID AAR66771 standard; protein; 435 AA.

AC AAR66771;

25-MAR-2003 (revised)

13-SEP-1995 (first entry)

Human interleukin-1 beta converging enzyme ced 3 homolog Ich-1(L).

Human interleukin-1 beta converting enzyme ced 3 homolog; Ich-1 (L);

[illegible]

OS
Homo sapiens.

PFH	Key	Location/Qualifiers
1	1-4-1	201 205

FT Active-Bite 301. .305

XX PN WO9500160-A1.
XX PD 05-JAN-1995.
XX PP 10-JUN-1994; 94WO-US006630.
XX PR 24-JUN-1993; 93US-00080850.
XX PA (GEHO) GEN HOSPITAL CORP.
XX PI Yuan J, Miura M;
XX DR WPI; 1995-051742/07.
XX PT N-PSDB; AAQ79971.
XX PS or preventing programmed cell death in vertebrate cells - by inhibiting
XX PT the activity of interleukin-1 beta converting enzyme.
XX PS Example 5; Fig 12A; 116pp; English.
XX CC AAQ79971 encodes AAR66771 human interleukin-1 beta converting enzyme ced
XX CC 3 homolog Ich-1(L), increasing Ich-1(L)s enzymatic activity can promote
XX CC the programmed cell death of cancer cells (pref. those overexpressing the
XX CC bcl-2 oncogene), this can be used as the basis of a new cancer treatment.
XX CC Alternatively by reducing Ich-1(L)s enzymatic activity programmed cell
XX CC death can be inhibited, this may be useful in the development of new cell
XX CC lines which remain viable in culture for extended or indefinite periods,
XX CC independent of growth factors. (Updated on 25-MAR-2003 to correct PN
XX CC field.)
XX SQ Sequence 435 AA;

Query Match 82.9%; Score 34; DB 2; Length 435;
Best Local Similarity 71.4%; Pred. NO. 9.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
Db 303 CRGDETD 309

RESULT 9
ID AAR98462
AC AAR98462; standard; protein; 435 AA.
XX 25-SEP-1996 (first entry)
XX Human Ice-ced-3 homologue-1L.
XX Ich-1L; human ICE-ced-3 homologue; programmed cell death; apoptosis;
XX interleukin-1 beta converting enzyme; gene therapy.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Domain 301-305
XX FT /label= QACED_active domain
XX PN WO9620721-A1.
XX PD 11-JUL-1996.
XX PF 04-JAN-1996; 96WO-US000177.
XX PR 04-JAN-1995; 95US-00368704.
XX PA (GEHO) GEN HOSPITAL CORP.
XX PI Yuan J, Miura M;
XX

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2005, 11:36:08 ; Search time 155.75 Seconds
(without alignments)
19.747 Million cell updates/sec

Title: US-09-473-619D-2
Perfect score: 41
Sequence: 1 CKGDEVD 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	7	2	AAW51893 Peptide u
2	37	90.2	103	8	ADY12242 Plant ful
3	36	87.8	385	5	AAO14833 Coffee th
4	36	87.8	385	5	AAO14834 Coffee th
5	34	82.9	21	8	ADM96249 Human cas
6	34	82.9	92	9	ADM95108 M. xanthu
7	34	82.9	379	8	ADJ71981 Human PMW
8	34	82.9	435	2	AAR66771 Human int
9	34	82.9	435	2	AAR98462 Human Ice
10	34	82.9	435	2	AAR90703 Interleuk
11	34	82.9	435	2	AAW26274 Cell deat
12	34	82.9	435	2	AAJ21716 Amino aci
13	34	82.9	435	3	AAAB14257 Human Ich
14	34	82.9	435	4	AAE00599 Human cas
15	34	82.9	435	5	ABW78321 Amino aci
16	34	82.9	435	5	ABJ01217 Human cas
17	34	82.9	435	7	ADG63002 Human Pro
18	34	82.9	435	7	ADL61332 Human apo
19	34	82.9	435	8	ADO16842 Human cas
20	34	82.9	435	9	AEC01583 Human CAS
21	34	82.9	441	2	AAR66768 Human int
22	34	82.9	441	3	ABA14253 Human Ich
23	34	82.9	452	5	ABJ01010 Mouse cas
24	34	82.9	452	7	ADB79812 Rat caspa

25	34	82.9	452	7	ADB63000	Ade63000 Rat Prote
26	33	80.5	19	4	AAG73096	Aag73096 Protease
27	33	80.5	55	4	AAU40501	Aau40501 Propionib
28	33	80.5	55	6	ABM37020	Abm37020 Propionib
29	33	80.5	165	8	ADQ65640	Adq65640 Novel hum
30	33	80.5	183	7	ADM65664	Adm65664 Na-ion ef
31	33	80.5	187	4	AAU20419	Aau20419 Human sec
32	33	80.5	212	4	ABG00310	Abg00310 Novel hum
33	33	80.5	212	7	ADC32771	Adc32771 Human nov
34	33	80.5	267	6	AAE35756	Aae35756 Human SEC
35	33	80.5	267	7	ADB65748	Adb65748 Human pro
36	33	80.5	267	7	ADC31054	Adc31054 Human nov
37	33	80.5	269	5	ABP51284	Abp51284 Human MDD
38	33	80.5	311	8	ADT61009	Adt61009 Plant pol
39	33	80.5	423	7	ABO83075	Abc83075 Pseudomon
40	33	80.5	450	4	ABB63682	Abb63682 Drosophil
41	33	80.5	625	6	ADA48492	Ada48492 Rice prot
42	33	80.5	2965	2	AAW56450	Aaw56450 Fragment
43	33	80.5	2969	2	AAW56447	Aaw56447 Fragment
44	33	80.5	2969	2	AAW56449	Aaw56449 Fragment
45	33	80.5	2969	2	AAW56446	Aaw56446 Fragment

ALIGNMENTS

RESULT 1
AAW51893
ID AAW51893 standard; peptide; 7 AA.
XX
AC AAW51893;
XX
DT 21-SEP-1998 (first entry)
XX
DE Peptide useful for diagnosing diseases that involve apoptosis.
XX
KW Immunogen; apoptosis; screen; inhibitor; stimulator; antibody; PARP;
KW poly-ADP-ribose polymerase; antibody.
XX
OS Mammalia.
XX
PN WO9821590-A1.
XX
PD 22-MAY-1998.
XX
PF 13-NOV-1997; 97WO-US020214.
XX
PR 15-NOV-1996; 96US-0030961P.
PR 12-NOV-1997; 97US-00967625.
XX (CEPH-) CEPHALON INC.
XX Siman R, Bozyczko-coyne D, Meyer SL, Bhat RV;
WPI; 1998-298113/26.
Peptide(s) containing epitope(s) characteristic of peptide(s) formed during apoptosis - useful for diagnosing diseases that involve apoptosis and to screen for inhibitors or stimulators of apoptosis.
Claim 1; Page 14; 40pp; English.
The invention relates to peptides that contain the sequences AAW51892-3. Also claimed are: (1) antibodies that bind specifically to an epitope on a peptide produced by apoptotic cells; (2) a method for identifying inhibitors or stimulators of apoptosis by measuring the effect of a test compound on amount of antibody bound to cell or tissue, and (3) kits for detecting peptides produced by apoptotic cells. Antibodies are used in immunoassays to detect and quantify apoptosis, particularly for diagnosis of apoptosis-associated conditions, e.g. chronic neurodegeneration, cancer, sepsis, trauma to head or spine, hypoxia, anoxia, ischaemia, lesions and exposure to toxins, or susceptibility to such a condition

SQ Sequence 7 AA;
 Query Match 100.0%; Score 41; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
 Db 1 CKGDEVD 7
 |||||

RESULT 2
 ADY12242
 ID ADY12242 standard; protein; 103 AA.
 XX
 AC ADY12242;
 XX
 DT 21-APR-2005 (first entry)
 XX
 DE Plant full length insert polypeptide seqid 68057.
 XX
 KW plant protectant; plant growth regulant; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content.
 XX
 OS Unidentified.
 XX
 EN US2004034888-A1.
 XX
 PD 19-FEB-2004.
 XX
 XX 28-APR-2003; 2003US-00425114.
 XX
 PF 06-MAY-1999; 99US-00304517.
 PR 05-NOV-2001; 2001US-00985678.
 XX
 XX (LIUJ/) LIU J.
 PA (ZHOU/) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREEN S E.
 PA (TABA/) TABASKA J E.
 PA (CAOY/) CAO Y.
 XX
 PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 XX WPI; 2004-180133/17.
 XX
 PT New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.
 XX
 PS Claim 1; SEQ ID NO 68057; 15pp; English.
 XX
 CC The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp:seqdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one

CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This is the amino acid sequence of a plant full length insert
 CC polypeptide that can be used in the recombinant DNA construct of the
 CC invention.
 XX SQ Sequence 103 AA;
 Query Match 90.2%; Score 37; DB 8; Length 103;
 Best Local Similarity 71.4%; Pred. No. 67;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
 Db 66 CRGDEID 72
 |||||

RESULT 3
 AAO14833
 ID AAO14833 standard; protein; 385 AA.
 XX
 AC AAO14833;
 XX
 DT 11-JUL-2002 (first entry)
 XX
 DE Coffee theobromine synthase-related protein (MTL1).
 XX
 KW Coffee; theobromine synthase; enzyme; 7-methylxanthine; caffeine;
 KW transgenic coffee plant; caffeineless coffee; MTL1;
 KW theobromine synthase-related protein.
 XX
 OS Coffea arabica.
 XX
 EN EPI197558-A2.
 XX
 PD 17-APR-2002.
 XX
 XX 27-SEP-2001; 2001EP-00122628.
 XX
 PF 06-OCT-2000; 2000JP-00307149.
 PR (NARA-) NARA INST SCI & TECHNOLOGY.
 XX
 XX Sano H, Kusano T, Koizumi N;
 XX WPI; 2002-354189/39.
 DR N-PSDB; AAL42628.
 XX
 PT New theobromine synthase polypeptide and encoding gene, useful for
 PT producing caffeineless coffee from transgenic plants having reduced
 PT expression of polypeptide.
 XX
 PS Example; Page 8; 19pp; English.
 XX
 CC The invention comprises the amino acid and coding sequence of the Coffea
 CC arabica (coffee) theobromine synthase enzyme. Theobromine synthase
 CC functions to catalyse the biosynthesis of theobromine from 7-
 CC methylxanthine. Caffeine is synthesised through N-methylation of the
 CC theobromine. The theobromine synthase gene is useful for preparing
 CC transformed coffee plants which have decreased expression of theobromine
 CC synthase - such plants can be used to produce caffeineless coffee. The
 CC theobromine synthase gene can also be used to produce transformed plants
 CC which have enhanced expression of theobromine. The present amino acid
 CC sequence represents a Coffea arabica theobromine synthase-related protein
 XX SQ Sequence 385 AA;
 Query Match 87.8%; Score 36; DB 5; Length 385;
 Best Local Similarity 85.7%; Pred. No. 3.7e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
 Db 228 CKGDECD 234
 |||||

RESULT 4

AAO14834
ID AAO14834 standard; protein; 385 AA.

XX
AC AAO14834;

XX
DT 11-JUL-2002 (first entry)

XX
DE Coffee theobromine synthase-related protein (MTL2).

XX
KW Coffee; theobromine synthase; enzyme; 7-methylxanthine; caffeine;

XX
KW transgenic coffee plant; caffeineless coffee; MTL2;

XX
KW theobromine synthase-related protein.

XX
OS Coffea arabica.

XX
PN EPI197558-A2.

XX
PD 17-APR-2002.

XX
PF 27-SEP-2001; 2001EP-00122628.

XX
PR 06-OCT-2000; 2000JP-00307149.

XX
PA (NARA-) NARA INST SCI & TECHNOLOGY.

XX
PI Sano H, Kusano T, Koizumi N;

XX
DR WPI; 2002-354189/39.

XX
DR N-PSDB; AAL42629.

XX
PT New theobromine synthase polypeptide and encoding gene, useful for
producing caffeineless coffee from transgenic plants having reduced
expression of polypeptide.

XX
PS Example; Page 9-10; 19pp; English.

XX
CC The invention comprises the amino acid and coding sequence of the Coffea
arabica (coffee) theobromine synthase enzyme. Theobromine synthase
functions to catalyze the biosynthesis of theobromine from 7-
methylxanthine. Caffeine is synthesised through N-methylation of the
theobromine. The theobromine synthase gene is useful for preparing
transformed coffee plants which have decreased expression of theobromine
synthase - such plants can be used to produce caffeineless coffee. The
theobromine synthase gene can also be used to produce transformed plants
which have enhanced expression of theobromine. The present amino acid
sequence represents a coffee arabica theobromine synthase-related protein

XX
SQ Sequence 385 AA;

Query Match 87.8%; Score 36; DB 5; Length 385;

Best Local Similarity 85.7%; Pred. No. 3.7e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7

Db 228 CKGDEFD 234

RESULT 5

ADM96249

ID ADM96249 standard; peptide; 21 AA.

XX
AC ADM96249;

XX
DT 15-JUL-2004 (first entry)

XX
DE Human caspase-2 peptide related to apoptosis modulation.

XX
KW apoptotic cell death; apoptotically active site; human alpha-fetoprotein;
human serum albumin; immunosuppressive; virucide;

KW apoptosis signaling modulator; apoptotic regulatory pathway;
organ preservation; cell preservation; transplantation;
KW autoimmune disorder; immunodeficiency syndrome; viral infection;
KW cytotoxicity; chemotherapy; radiotherapy; neuronal cell apoptosis;
KW non-specific drug-induced apoptosis; oxidative stress-mediated apoptosis;
KW cultured cell apoptosis; caspase-2; human.

OS Homo sapiens.

XX
PN WO2004033500-A1.

XX
PD 22-APR-2004.

XX
PF 07-OCT-2003; 2003WO-FI000735.

XX
PR 09-OCT-2002; 2002FI-00001798.

XX
PA (DUDI/) DUDICH E I.

XX
PA (SEME/) SEMENKOVA L N.

XX
PA (DUDI/) DUDICH I V.

XX
PA (TATU/) TATULOV E B.

XX
PA (ZUBO/) ZUBOV D L.

XX
PA (KORP/) KORPELA T K.

XX
PI Dudich EI, Semenkova LN, Dudich IV, Tatulov EB, Zubov DL;

XX
PI Korpela TK;

XX
DR WPI; 2004-340893/31.

XX
PT New molecular structure of the recognition site of an anti-idiotypic
antibody against an apoptotically active site of human alpha-fetoprotein,
useful for preventing of autoimmune disorders and an immunodeficiency
syndrome.

XX
PS Example 2; Page 13; 36pp; English.

XX
CC This invention relates to novel peptides capable of modulating apoptotic
cell death. In particular, the invention relates to the molecular
structure of the apoptotically active site of human alpha-fetoprotein and
human serum albumin. The invention may be useful for the development of
compounds with an immunosuppressive or virucide activity acting as
apoptosis signaling modulators. The peptide structures are useful for
suppressing apoptotic regulatory pathways in human and animal cells, for
increasing preservation of organs or cells within their transplantation,
for preventing of autoimmune disorders and an immunodeficiency syndrome
induced by a viral infection, for lowering cytotoxic effects after chemo
or radiotherapy, for inhibiting neuronal cell apoptosis, non-specific
drug-induced apoptosis or oxidative stress-mediated apoptosis, and for
preventing apoptosis of cultured cells prepared for scientific or
technical purposes. The present sequence is that of a human caspase-2
peptide which was used in the exemplification of the invention.

XX
SQ Sequence 21 AA;

Query Match 82.9%; Score 34; DB 8; Length 21;

Best Local Similarity 71.4%; Pred. No. 48;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7

Db 12 CRGDETD 18

RESULT 6

ABM95108

ID ABM95108 standard; protein; 92 AA.

XX
AC ABM95108;

XX
DT 02-JUN-2005 (first entry)

XX
DE M. xanthus protein sequence, seq id 14307.

XX

KW Transgenic plant; DNA replication; gene regulation; gene expression.
 XX Myxococcus xanthus.
 OS
 XX
 XX
 FN US6833447-B1.
 XX
 XX
 PD 21-DEC-2004.
 XX
 XX
 PF 10-JUL-2001; 2001US-00902540.
 XX
 XX
 PR 10-JUL-2000; 2000US-0217883P.
 XX
 XX (MONS) MONSANTO TECHNOLOGY LLC.
 PA
 XX
 XX Goldman BS, Hinkle GJ, Slater SC, Wiegand RC;
 PI
 XX
 XX WPI; 2005-028716/03.
 DR
 XX
 XX New substantially purified Myxococcus xanthus nucleic acid molecule
 PT encoding a nitrite reductase, useful for determining gene expression,
 PT identifying mutations in a gene of interest, and for constructing
 PT mutations in a gene of interest.
 XX
 XX Example 2; SEQ ID NO 14307; 25pp; English.
 PS
 XX
 XX The invention relates to a substantially purified nucleic acid molecule
 CC encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a
 CC recombinant DNA construct for expression of a nitrite reductase gene in a
 CC plant cell, and a plant cell comprising the recombinant DNA construct.
 CC The nucleic acid is useful for determining gene expression, identifying
 CC mutations in a gene of interest, and for constructing mutations in a gene
 CC of interest. Sequences given in records for SEQ IDs 9692-16825 represent
 CC a group of 7134 Myxococcus xanthus proteins and peptides. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from USPTO
 XX
 XX Sequence 92 AA;
 Query Match 82.9%; Score 34; DB 9; Length 92;
 Best Local Similarity 71.4%; Pred. No. 2.1e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CKGDEVD 7
 |||||
 Db 68 CKGDDAD 74
 RESULT 7
 ADJ71981
 ID ADJ71981 standard; protein; 379 AA.
 XX
 XX ADJ71981;
 XX
 XX 06-MAY-2004 (first entry)
 DT
 XX
 XX Human PMMM protein amino acid sequence SeqID41.
 DE
 XX protein modification and maintenance molecule; PMMM; cytostatic;
 KW antiarteriosclerotic; anticonvulsant; nootropic; neuroprotective;
 KW cerebroprotective; vasotropic; anti-HIV; antiallergic; antimicrobial;
 KW anti-inflammatory; endocrine-Gen; thyromimetic;
 KW cell proliferative disorder; cancer; atherosclerosis;
 KW neurological disorder; epilepsy; Huntington's disease; stroke;
 KW immune disorder; inflammatory disorder; AIDS; allergy;
 KW developmental disorder; Hypothyroidism; Cushing's syndrome; infection;
 KW human.
 XX
 XX Homo sapiens.
 OS
 XX WO2004009797-A2.
 FN
 XX
 XX 29-JAN-2004.
 PD
 XX

PF 23-JUL-2003; 2003WO-US023249.
 XX
 XX 23-JUL-2002; 2002US-0398143P.
 PR 09-AUG-2002; 2002US-0402458P.
 PR 12-AUG-2002; 2002US-0403289P.
 PR 27-AUG-2002; 2002US-0406472P.
 PR 06-SEP-2002; 2002US-0409354P.
 XX
 XX (INCY-) INCYTE CORP.
 PA
 XX Elliott VS, Swarnakar A, Griffin JA, Lee EA, Sprague WW;
 PI Hafalia AJA, Lee SY, Kable AE, Ison CH, Khare R, Chawla NK;
 PI Marquis JP, Jiang X, Jackson AA, Becha SD, Emerling BM, Jin P;
 PI Wilson AD, Richardson TW, Yang J, Baughn WR, Gandhi AR, Nguyen DB;
 PI Ramkumar J, Kallick DA, Kearney L, Lu DAM, Gietzen KJ, Tribouley CM;
 PI Lal PG, Blake JJ, Lu Y, Arvizu CS;
 XX
 XX WPI; 2004-123392/12.
 DR
 DR N-PSDB; ADJ72043.
 XX
 XX New human protein modification and maintenance molecules (PMMM), useful
 PT for diagnosing, treating and preventing diseases or conditions associated
 PT with the aberrant PMMM expression e.g. cancer, AIDS, epilepsy, or
 PT infections.
 XX
 XX Claim 1; SEQ ID NO 41; 387pp; English.
 PS
 XX
 XX This invention relates to novel protein modification and maintenance
 CC molecules (PMMM) and polynucleotides which identify and encode PMMM. The
 CC invention may be useful for the development of compositions with a
 CC cytostatic, antiarteriosclerotic, anticonvulsant, nootropic,
 CC neuroprotective, cerebroprotective, vasotropic, anti-HIV, antiallergic,
 CC antimicrobial, anti-inflammatory, endocrine-Gen or thyromimetic activity.
 CC The polypeptides and polynucleotides are useful in diagnosing, treating
 CC and preventing diseases or conditions associated with the decreased
 CC expression or overexpression of PMMM, such as cell proliferative (for
 CC example cancer, atherosclerosis), neurological (for example epilepsy,
 CC Huntington's disease, stroke), immune/inflammatory (for example AIDS,
 CC allergies) and developmental (for example Hypothyroidism, Cushing's
 CC syndrome) disorders, or infections. These are also useful in assessing
 CC the effects of exogenous compounds on the expression of nucleic acid and
 CC amino acid sequences of PMMM. The present sequence is that of a human
 CC PMMM protein of the invention.
 XX
 XX Sequence 379 AA;
 Query Match 82.9%; Score 34; DB 8; Length 379;
 Best Local Similarity 71.4%; Pred. No. 8.3e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CKGDEVD 7
 |||||
 Db 303 CRGDETD 309
 RESULT 8
 AAR66771
 ID AAR66771 standard; protein; 435 AA.
 XX
 XX AAR66771;
 AC
 XX 25-MAR-2003 (revised)
 DT
 DT 13-SEP-1995 (first entry)
 XX
 XX Human interleukin-1 beta convering enzyme ced 3 homolog Ich-1(L).
 DE
 XX Human interleukin-1 beta converitng enzyme ced 3 homolog; Ich-1(L);
 KW oncogene bcl-2; programmed cell death; cancer treatment.
 XX
 XX Homo sapiens.
 OS
 XX WO2004009797-A2.
 FN
 XX
 XX 29-JAN-2004.
 PD
 XX

```

XX FN WO9500160-A1.
XX PD 05-JAN-1995.
XX PF 10-JUN-1994; 94WO-US006630.
XX PR 24-JUN-1993; 93US-00080850.
XX PA (GEO) GEN HOSPITAL CORP.
XX PI Yuan J, Miura M;
XX PI WPI; 1995-051742/07.
DR N-PSDB; AAR97971.
XX or preventing programmed cell death in vertebrate cells - by inhibiting
PT the activity of interleukin-1 beta converting enzyme.
XX Example 5; Fig 12A; 116pp; English.
XX AAQ79971 encodes AAR66771 human interleukin-1 beta converting enzyme ced
CC 3 homolog Ich-1(L), increasing Ich-1(L)s enzymatic activity can promote
CC the programmed cell death of cancer cells (pref. those overexpressing the
CC bcl-2 oncogene), this can be used as the basis of a new cancer treatment.
CC Alternatively by reducing Ich-1(L)s enzymatic activity programmed cell
CC death can be inhibited, this may be useful in the development of new cell
CC lines which remain viable in culture for extended or indefinite periods,
CC independent of growth factors. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX SQ Sequence 435 AA;

Query Match 82.9%; Score 34; DB 2; Length 435;
Best Local Similarity 71.4%; Pred. No. 9.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
Db 303 CRGDETD 309

RESULT 9
AAR98462
ID AAR98462 standard; protein; 435 AA.
XX AAR98462;
AC AAR98462;
XX 25-SEP-1996 (first entry)
XX Human Ice-ced-3 homologue-1L.
XX Ich-1L; human ICE-ced-3 homologue; programmed cell death; apoptosis;
KW interleukin-1 beta converting enzyme; gene therapy.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Domain 301..305
FT /label= QACRG_active_domain
XX WO9620721-A1.
XX 11-JUL-1996.
XX 04-JAN-1996; 96WO-US000177.
XX 04-JAN-1995; 95US-00368704.
XX (GEO) GEN HOSPITAL CORP.
XX Yuan J, Miura M;

```

```

DR N-PSDB; AAT31552.
XX Preventing or promoting programmed cell death in vertebrate cells -
PT comprises inhibiting or increasing the activity of interleukin-1-beta
PT converting enzyme, or altering expression of other related genes.
XX Claim 19; Fig 10A; 127pp; English.
XX A novel human cell death gene, designated Ich-1 (ICE-ced-3 homologue-1),
CC was identified as a new member of the ced-3/ICE family. Ich-1 is
CC alternatively spliced into 2 different forms. Ich-1L cDNA (AAT31552)
CC encodes a 435-amino acid protein (AAR98462) that is homologous to the P20
CC and P10 subunits of human interleukin-1 beta converting enzyme (ICE). Ich
CC -1S cDNA (AAT31553) encodes a 312-amino acid protein (AAR98463) that is a
CC truncated version of Ich-1L that terminates 21 residues after the QACRG
CC active domain of Ich-1L. Overexpression of Ich-1L induces Rat-1
CC fibroblast cells to die in culture, but overexpression of Ich-1S
CC suppresses Rat-1 cell death. Ich-1L and Ich-1S are useful in methods of
CC controlling programmed cell death of vertebrate cells
XX SQ Sequence 435 AA;

Query Match 82.9%; Score 34; DB 2; Length 435;
Best Local Similarity 71.4%; Pred. No. 9.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
Db 303 CRGDETD 309

RESULT 10
AAR90703
ID AAR90703 standard; protein; 435 AA.
XX AAR90703;
AC AAR90703;
XX 10-APR-1996 (first entry)
XX Interleukin-1-beta converting enzyme like apoptosis protease-2.
XX Interleukin-1-beta converting enzyme like apoptosis protease-2;
KW ICE-LAP-2; cell death; immunosuppression; AIDS; Alzheimer disease;
KW Parkinson disease; septic shock; rheumatoid arthritis; head injury;
KW antitumour; antiviral.
XX Homo sapiens.
XX WO9600297-A1.
XX 04-JAN-1996.
XX 23-JUN-1994; 94WO-US007127.
XX 23-JUN-1994; 94WO-US007127.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Wei WH, Craig AR, Hastings GA, Hudson PL, Kirkness EF;
XX N-PSDB; AAT15579.
XX Interleukin-1 beta converting enzyme like apoptosis protease-1 and -2 -
PT controls programmed cell death, used in treatment of immunosuppression
PT related disorders, e.g. AIDS and Alzheimer's disease.
XX Claim 1; Fig 2A-C; 58pp; English.
XX Human interleukin-1-beta converting enzyme like apoptosis protease-2 (ICE
CC -LAP-2) (AAR90703) is structurally related interleukin-1-beta converting
CC enzyme, which is responsible for apoptosis. Recombinant ICE-LAP-2 is

```

CC obtd. by expression of encoding cDNA (AAT15579) in procarcynotic or
 CC eucaryotic host cells. It is used to treat diseases related to abnormally
 CC controlled programmed cell death, to control vertebrate development and
 CC tissue homeostasis, to overcome viral infections and to treat
 CC immunosuppression-related disorders
 XX
 SQ Sequence 435 AA;

Query Match 82.9%; Score 34; DB 2; Length 435;
 Best Local Similarity 71.4%; Pred. No. 9.5e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
 |:|||||
 Db 303 CRGDETD 309

RESULT 11

AAW26274
 ID AAW26274 standard; protein; 435 AA.

XX
 AC AAW26274;

XX 14-APR-1998 (first entry)

XX Cell death protein ICH-11.

XX cell death; ICH-11; interleukin-1 beta; apoptosis; treatment; IL-1;
 KW tumour; oncogenic transformation; IL-1 receptor antagonist; IL-1RA;
 KW IL-1 beta.

XX Homo sapiens.

XX WO9733606-A1.

XX 18-SEP-1997.

XX 15-MAR-1996; 96WO-US003468.

XX 15-MAR-1996; 96WO-US003468.

XX (GEO) GEN HOSPITAL CORP.

XX Yuan J, Friedlander R;

XX WPI; 1997-470641/43.

XX N-PSDB; AAT90565.

XX Preventing apoptosis by blocking binding of interleukin-1beta to its
 PT receptor - useful for, e.g. treating tumours, and inhibiting oncogenic
 PT transformation.

XX Example 5; Fig 7; 42pp; English.

XX This is a cell death protein ICH-11. The cell death caused by this ICH-11
 CC can be prevented by a new method using IL-1 receptor antagonist (IL-1RA).
 CC IL-1RA is also used in a method for preventing programmed cell death by
 CC blocking the binding of interleukin-1 beta (IL-1 beta) to its receptor.
 CC Other methods for modulating programmed cell death are provided in the
 CC specification like a method of modulating apoptosis by activating the IL-
 CC 1 beta converting enzyme (ICE) pathway and IL-1 beta production, a method
 CC for altering levels of hypoxia-induced cell death by blocking IL-1-
 CC mediated signal transduction, a method for killing oncogenically
 CC transformed cells by stimulating apoptosis with IL-1 beta or tumour
 CC necrosis factor alpha (TNF alpha), a method of inhibiting hypoxia-induced
 CC cell death by transfecting cells with the Crma gene (of cowpox), and a
 CC method for modulating apoptosis by downregulating the IL-1 receptor. IL-
 CC 1RA inhibits apoptosis induced by trophic factor depletion or hypoxia.
 CC while mature IL-1 beta induces cell death through a pathway independent
 CC of Crma-sensitive gene activity, and cooperates with ICE and ICH-11 in
 CC apoptosis. Pro-IL-1 beta is the first substrate of any apoptosis-inducing
 CC gene. Increasing/decreasing cells death can be used for the treatment of
 CC tumours (or other conditions where apoptosis is involved). Altering cell

CC death can also be used for inhibiting oncogenic transformation, and to
 CC treat complications involving apoptosis in cases of hypoxia or ischaemia.
 CC The methods can also be used to screen for agents that modulate
 CC apoptosis. When IL-1 beta is produced endogenously (via ICE) it mediates
 CC cell death, but when added exogenously it may stimulate death if it binds
 CC to its receptor after application of apoptotic stimulus or inhibit it by
 CC binding to the receptor before application of the stimulus
 XX

SQ Sequence 435 AA;

Query Match 82.9%; Score 34; DB 2; Length 435;
 Best Local Similarity 71.4%; Pred. No. 9.5e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
 |:|||||
 Db 303 CRGDETD 309

RESULT 12

AAW21716

ID AAY21716 standard; protein; 435 AA.

XX
 AC AAY21716;

XX 10-SEP-1999 (first entry)

XX Amino acid sequence of caspase-2 (ICH-1).

XX Rev-caspase; cysteine protease; zymogen; caspase; cancer; gene therapy;
 KW autoimmune disease; caspase-mediated apoptosis; neurodegenerative;
 KW tumour cell; myocardial infarction; human.

XX Homo sapiens.

XX WO9935277-A2.

XX 15-JUL-1999.

XX 11-JAN-1999; 99WO-US000632.

XX 09-JAN-1998; 98US-0070987P.

XX (UVJE-) UNIV JEFFERSON THOMAS.

XX Alnemri ES;

XX WPI; 1999-419353/35.

XX N-PSDB; AAX81218.

XX New isolated nucleic acid molecule encoding a rev-caspase - used for
 PT screening and identifying inhibitors or enhancers for treating cancer or
 PT autoimmune disease.

XX Disclosure; Fig 12A-B; 74pp; English.

XX The invention relates to nucleic acid molecules encoding rev-caspases.
 CC Rev-caspases are cysteine proteases that specifically cleave proteins
 CC after Asp residues and is expressed as a zymogen, in which the small
 CC subunit is N-terminal to a large subunit. A gene delivery vehicle
 CC comprising a rev-caspase coding sequence is useful for the treatment of
 CC cancer, where the gene delivery vehicle is internalised by tumour cells.
 CC The gene delivery vehicle can also be used to treat autoimmune diseases.
 CC Cells transfected with a rev-caspase expressing vector can be used in
 CC identification of inhibitors or enhancers of caspase-mediated apoptosis.
 CC In vitro translated rev-caspase can be used to identify an inhibitor or
 CC enhancer of caspase processing activity. Caspase inhibitors are useful
 CC for treating neurodegenerative diseases as well as for inhibiting
 CC apoptosis in the heart following myocardial infarction. Sequences
 CC AAX81217 -AAX81226 represent human caspase genes encoding caspase 1-10
 CC gene products (AAY21715-Y21724)

XX Sequence 435 AA;

Query Match 82.9%; Score 34; DB 2; Length 435;
Best Local Similarity 71.4%; Pred. No. 9.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKGDEVD 7
|:|:|:|
Db 303 CRGDETD 309

RESULT 13

AAB14257
ID AAB14257 standard; protein; 435 AA.

XX AC AAB14257;

XX 09-FEB-2001 (first entry)

XX Human Ich-1L protein sequence.

XX ced-3; virally induced cell death; apoptosis; gene therapy; neural;
KW muscular degenerative disease; myocardial infarction; stroke; aging;
KW interleukin-beta converting enzyme; Ich-1L; human; ICE.

XX Homo sapiens.

XX US6083735-A.

XX 04-JUL-2000.

XX 10-JUN-1994; 94US-00258287.

XX 24-JUN-1993; 93US-00080850.

XX (GEHO) GEN HOSPITAL CORP.

XX Yuan J, Miura M;

XX WPI; 2000-464343/40.

XX N-PSDB; AAA72841.

XX New human Ich-1L and Ich-1S proteins for negative and positive regulation
PT of programmed cell death and for developing therapeutic methods for
PT diseases and conditions characterized by cell death, e.g. myocardial
PT infarction or stroke.

XX Claim 1; Fig 12; 121pp; English.

XX The present sequence is a human Ice-ced 3 homologue (Ich-1) protein. The
CC present sequence is a member of a family of genes involved in programmed
CC cell death (apoptosis). The other family members include: the ced-3 gene
CC of C. elegans (AAA72802), human interleukin-1beta converting enzyme (ICE)
CC (AAB14250), murine ICE1 (AAB14249), and murine ICE2 (AAB14252). Ich-1
CC mRNA is alternatively spliced into two different forms. One alternative
CC transcript encodes the present protein, Ich-1L. The other mRNA encodes a
CC protein product of 312 amino acids, Ich-1S (AAB14258). Expression of Ich-
CC 1L and Ich-1S have opposite effects on cell death. Overexpression of Ich-
CC 1L induces cell death, while overexpression of Ich-1S suppresses cell
CC death induced by serum deprivation. Therefore, Ich-1 may play an
CC important role in both the positive and negative regulation of apoptosis.
CC The Ich gene may be used in gene therapy in disorders characterised by
CC cell death e.g. neural and muscular degenerative diseases, myocardial
CC infarction, stroke, virally induced cell death and aging

XX Sequence 435 AA;

Query Match 82.9%; Score 34; DB 3; Length 435;
Best Local Similarity 71.4%; Pred. No. 9.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKGDEVD 7
|:|:|:|
Db 303 CRGDETD 309

RESULT 14

AAE00599
ID AAE00599 standard; protein; 435 AA.

XX AC AAE00599;

XX 02-JUL-2001 (first entry)

XX Human caspase-2, alternative version.

XX Human; caspase-2; Ich1; urokinase; proliferation; gene therapy;
KW cysteine protease; apoptosis; caspase expression cassette; metastasis;
KW tumour; cathepsin B.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 1..14
/note= "Amino acid residues found in this sequence are
absent in the sequence shown in page 83-85 (AAE00616) "

FT Misc-difference 1..9
/note= "Encoded by ATA"

FT Misc-difference 305..307
/note= "Encoded by GGAGTGTATTGGATCCCTTGGGCACCTCCTTCT
GTTACATGCTGCCACCCCTCTCTGTCTATGAG"

FT Cleavage-site 316..317
/label= Proteolytic_cleavage_site

XX WO200129232-A2.

XX 26-APR-2001.

XX 19-OCT-2000; 2000WO-US028941.

XX 20-OCT-1999; 99US-0160559P.

XX 14-AUG-2000; 2000US-0225564P.

XX (SCIO-) SCIOS INC.

XX Cordell B, Li Y;

XX WPI; 2001-290920/30.

XX N-PSDB; AAD03909.

XX Novel fusion polypeptide comprising first and second caspase subunit
PT separated by cleavage site not associated in nature with caspase subunit,
PT useful for cloning gene encoding enzymes involved in proteolytic
PT cleavage.

XX Claim 4; Fig 4; 116pp; English.

XX The present sequence is an alternative version of human Caspase-2 also
CC known as Ich-1. Caspases are a family of cysteine proteases, that
CC participate in the initiation and execution of apoptosis. Caspases exist
CC as pro-enzymes, activated by cleavage into a large and small subunit,
CC occurring after specific aspartic acid residues within the pro-enzyme
CC sequence. The present invention relates to a method for functional
CC cloning of genes encoding proteins or enzymes involved in proteolytic
CC cleavage. The invention is based on the use of caspase expression
CC cassettes comprising the coding sequence of a proteolytic cleavage site
CC flanked by sequences encoding two caspase subunits. A fusion polypeptide
CC comprising a first and a second caspase subunit, separated by a cleavage
CC site not associated in nature, is useful for cloning gene encoding
CC enzymes involved in proteolytic cleavage. An expression cassette
CC containing fusion polypeptide is used to identify a mutant cell line
CC deficient in an enzyme of interest and is also useful for diagnosis and
CC suppression of proliferation or metastases of a tumour cell characterised
CC by overexpression of a polypeptide (e.g. Cathepsin B or urokinase,
CC selectively expressed in the tumour cells). DNA encoding fusion
CC polypeptide is used in gene therapy. Note: This sequence SEQ.ID.NO.4 is
CC stated as being the same as that shown in page 83-85 (See AAE00616) in

CC the specification. However these sequences differ at several positions
 XX
 SQ Sequence 435 AA;

Query Match 82.9%; Score 34; DB 4; Length 435;
 Best Local Similarity 71.4%; Pred. No. 9.5e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
 |:|||
 Db 303 CRGDETD 309

RESULT 15

ABB7832I
 ID ABB78321 standard; protein; 435 AA.

XX AC ABB78321;

XX DT 05-DEC-2002 (first entry)

XX DE Amino acid sequence of ICH-1L, a cell death protein.

XX KW Programmed cell death; apoptosis; interleukin-1beta receptor;
 KW IL-1beta receptor; tumour; ICH-1L; cell death protein.

XX OS Unidentified.

XX FN US6416753-B1.

XX PD 09-JUL-2002.

XX PF 13-MAR-1997; 97US-00816075.

XX PR 15-MAR-1996; 96US-0013524P.

XX PA (GEO) GEN HOSPITAL CORP.

XX PI Yuan J, Friedlander R;

XX DR WPI; 2002-634725/68.

XX DR N-PSDB; ABV72260.

XX PT Inhibiting programmed cell death (apoptosis) for treating tumors,
 PT involves providing an agent that blocks interleukin-1 beta receptor
 PT binding to a cell or cells, and inhibiting programmed cell death.

XX PS Disclosure; Fig 7A-C; 26pp; English.

XX CC The specification describes a method for inhibiting programmed cell death
 CC (apoptosis). The method comprises providing an agent that blocks
 CC interleukin-1beta (IL-1beta) receptor binding to a cell or cells, and
 CC inhibiting programmed cell death. The method is useful for inhibiting
 CC programmed cell death of vertebrate cells. It is useful for treating
 CC various pathologies including tumours of specific body organs of animal
 CC including human. The present sequence represents ICH-1L, a cell death
 CC protein

XX SQ Sequence 435 AA;

Query Match 82.9%; Score 34; DB 5; Length 435;
 Best Local Similarity 71.4%; Pred. No. 9.5e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
 |:|||
 Db 303 CRGDETD 309

Search completed: December 27, 2005, 11:43:20
 Job time : 158.75 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2005, 11:36:08 ; Search time 26.8333 Seconds
(without alignments)
25.100 Million cell updates/sec

Title: US-09-473-619D-2

Perfect score: 41

Sequence: 1 CKGDEVD 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues , 283416
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_80.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	82.9	182	2	I67436
2	34	82.9	352	2	interleukin-1-beta
3	34	82.9	352	2	hypothetical prote
4	34	82.9	361	2	probable ABC trans
5	34	82.9	435	2	bromodomain protei
6	34	82.9	452	2	apoptosis regulato
7	33	80.5	219	2	caspase-2 - rat
8	33	80.5	878	2	pentose-5-phosphat
9	32	78.0	209	2	valine-tRNA ligase
10	32	78.0	514	2	protein T12C24.14
11	32	78.0	780	2	hypothetical prote
12	32	78.0	826	2	ATP-dependent DNA
13	32	78.0	996	2	caspase-related pr
14	32	78.0	1013	1	import intermediat
15	32	78.0	1014	1	NAD ADP-ribosyltra
16	32	78.0	1016	1	NAD ADP-ribosyltra
17	32	78.0	1131	2	hypothetical prote
18	32	78.0	1556	2	glutamate synthase
19	31	75.6	142	2	hypothetical prote
20	31	75.6	152	2	hypothetical prote
21	31	75.6	182	2	conserved hypothet
22	31	75.6	189	2	anthranilate synth
23	31	75.6	240	2	transcription regu
24	31	75.6	382	2	serum albumin - bu
25	31	75.6	385	2	major surface prot
26	31	75.6	393	1	Ig mu chain C regi
27	31	75.6	396	2	glutaminl-tRNA redu
28	31	75.6	404	2	hypothetical prote
29	31	75.6	420	2	dnaj protein homol

30	31	75.6	420	2	T49127
31	31	75.6	438	1	HVRKCS
32	31	75.6	461	1	HVRKCO
33	31	75.6	469	2	S45453
34	31	75.6	541	2	S56653
35	31	75.6	548	2	T22137
36	31	75.6	596	2	A96710
37	31	75.6	661	2	F96665
38	31	75.6	773	2	E71931
39	31	75.6	773	2	E64582
40	31	75.6	782	2	I48746
41	31	75.6	784	2	T26585
42	31	75.6	953	2	I48078
43	31	75.6	960	1	S28262
44	31	75.6	1097	2	G85092
45	31	75.6	1213	2	A54063

ALIGNMENTS

RESULT 1

I67436

interleukin-1-beta-converting enzyme and ced-3 homolog-1, long isoform - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)

C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004

C;Accession: I67436

R;Flaws, J.A.; Kugu, K.; Trbovich, A.M.; DeSanti, A.; Tilly, K.I.; Hirshfield, A.N.; Tilly

Endocrinology 136, 5042-5053, 1995

A;Title: Interleukin-1-beta-converting enzyme-related proteases (IRPs) and mammalian cell

nulosa cells of the ovarian follicle.

A;Reference number: 153300; MUID:96042508; PMID:7588240

A;Accession: I67436

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 1-182 <RES>

A;Cross-references: UNIPROT:P55215; UNIPARC:UPI00001707FB; EMBL:U34684; NID:G1004368; PII

Query Match 82.9%; Score 34; DB 2; Length 182;

Best Local Similarity 71.4%; Pred. No. 29;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7

|:|:|:|

Db 123 CRGDETD 129

RESULT 2

A12884

hypothetical protein Atu2508 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens

C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004

C;Accession: A12884

R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, F

ster, E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2577; MUID:21608550; PMID:11743193

A;Accession: A12884

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-352 <KUR>

A;Cross-references: UNIPROT:Q8UCH9; UNIPARC:UPI00000D1F1B; GB:AE008688; PIDN:AAL43495.1;

A;Experimental source: strain C58 (Dupont)

C;Genetics:

A;Gene: Atu2508

A;Map position: circular chromosome

C;Superfamily: inner membrane protein malK; ATP-binding cassette homology

Query Match 82.9%; Score 34; DB 2; Length 352;

Best Local Similarity 83.3%; Pred. No. 53;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CKGDEV 6
Db 311 CKGDEI 316

RESULT 3
F97660
Probable ABC transporter ATP-binding protein y40S AGR_C_4558 [imported] - Agrobacterium
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: F97660
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: F97660
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-352 <KUR>
A;Cross-references: UNIPROT:Q8UCH9; UNIPARC:UPI000000D1F1B; GB:AE007869; PIDN:AAK88239.1;
C;Genetics:
A;Gene: AGR_C_4558
A;Map position: circular chromosome
C;Superfamily: inner membrane protein malK; ATP-binding cassette homology

Query Match 82.9%; Score 34; DB 2; Length 352;
Best Local Similarity 83.3%; Pred. No. 53;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CKGDEV 6
Db 311 CKGDEI 316

RESULT 4
T42517
bromodomain protein - fission yeast (Schizosaccharomyces pombe) (fragment)
C;Species: Schizosaccharomyces pombe
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T42517
R;Yoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
DNA Res. 4, 363-369, 1997
A;Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
A;Reference number: Z17323; MUID:98162722; PMID:9501991
A;Accession: T42517
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-361 <YOS>
A;Cross-references: UNIPROT:Q9HGP4; UNIPARC:UPI00000069D9D; EMBL:D89157; NID:gl749521; PI
A;Experimental source: strain PR745
F;64-121/Domain: bromodomain homology <BRO>

Query Match 82.9%; Score 34; DB 2; Length 361;
Best Local Similarity 83.3%; Pred. No. 54;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CKGDEV 6
Db 288 CKGDEI 293

RESULT 5
A54821
apoptosis regulator ICH-1, stimulatory form L - human
C;Species: Homo sapiens (man)
C;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 09-Jul-2004
C;Accession: A54821
R;Wang, L.; Miura, M.; Bergeron, L.; Zhu, H.; Yuan, J.
Cell 78, 739-750, 1994

Best Local Similarity 83.3%; Pred. No. 53;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CKGDEV 6
Db 311 CKGDEI 316

RESULT 3
F97660
Probable ABC transporter ATP-binding protein y40S AGR_C_4558 [imported] - Agrobacterium
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: F97660
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: F97660
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-352 <KUR>
A;Cross-references: UNIPROT:Q8UCH9; UNIPARC:UPI000000D1F1B; GB:AE007869; PIDN:AAK88239.1;
C;Genetics:
A;Gene: AGR_C_4558
A;Map position: circular chromosome
C;Superfamily: inner membrane protein malK; ATP-binding cassette homology

Query Match 82.9%; Score 34; DB 2; Length 352;
Best Local Similarity 83.3%; Pred. No. 53;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CKGDEV 6
Db 311 CKGDEI 316

RESULT 4
T42517
bromodomain protein - fission yeast (Schizosaccharomyces pombe) (fragment)
C;Species: Schizosaccharomyces pombe
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T42517
R;Yoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
DNA Res. 4, 363-369, 1997
A;Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
A;Reference number: Z17323; MUID:98162722; PMID:9501991
A;Accession: T42517
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-361 <YOS>
A;Cross-references: UNIPROT:Q9HGP4; UNIPARC:UPI00000069D9D; EMBL:D89157; NID:gl749521; PI
A;Experimental source: strain PR745
F;64-121/Domain: bromodomain homology <BRO>

Query Match 82.9%; Score 34; DB 2; Length 361;
Best Local Similarity 83.3%; Pred. No. 54;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CKGDEV 6
Db 288 CKGDEI 293

RESULT 5
A54821
apoptosis regulator ICH-1, stimulatory form L - human
C;Species: Homo sapiens (man)
C;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 09-Jul-2004
C;Accession: A54821
R;Wang, L.; Miura, M.; Bergeron, L.; Zhu, H.; Yuan, J.
Cell 78, 739-750, 1994

Best Local Similarity 83.3%; Pred. No. 53;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CKGDEV 6
Db 311 CKGDEI 316

RESULT 3
F97660
Probable ABC transporter ATP-binding protein y40S AGR_C_4558 [imported] - Agrobacterium
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: F97660
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: F97660
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-352 <KUR>
A;Cross-references: UNIPROT:Q8UCH9; UNIPARC:UPI000000D1F1B; GB:AE007869; PIDN:AAK88239.1;
C;Genetics:
A;Gene: AGR_C_4558
A;Map position: circular chromosome
C;Superfamily: inner membrane protein malK; ATP-binding cassette homology

Query Match 82.9%; Score 34; DB 2; Length 352;
Best Local Similarity 83.3%; Pred. No. 53;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CKGDEV 6
Db 311 CKGDEI 316

RESULT 4
T42517
bromodomain protein - fission yeast (Schizosaccharomyces pombe) (fragment)
C;Species: Schizosaccharomyces pombe
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T42517
R;Yoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
DNA Res. 4, 363-369, 1997
A;Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
A;Reference number: Z17323; MUID:98162722; PMID:9501991
A;Accession: T42517
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-361 <YOS>
A;Cross-references: UNIPROT:Q9HGP4; UNIPARC:UPI00000069D9D; EMBL:D89157; NID:gl749521; PI
A;Experimental source: strain PR745
F;64-121/Domain: bromodomain homology <BRO>

Query Match 82.9%; Score 34; DB 2; Length 361;
Best Local Similarity 83.3%; Pred. No. 54;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CKGDEV 6
Db 288 CKGDEI 293

RESULT 5
A54821
apoptosis regulator ICH-1, stimulatory form L - human
C;Species: Homo sapiens (man)
C;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 09-Jul-2004
C;Accession: A54821
R;Wang, L.; Miura, M.; Bergeron, L.; Zhu, H.; Yuan, J.
Cell 78, 739-750, 1994

A;Title: Ich-1, an Ice/ced-3-related gene, encodes both positive and negative regulators
A;Reference number: A54821; MUID:94373811; PMID:8087842
A;Accession: A54821
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-435 <WAN>
A;Cross-references: UNIPROT:P42575; UNIPARC:UPI000000D909; GB:U13021; NID:g537291; PID:g5
C;Keywords: alternative splicing; apoptosis

Query Match 82.9%; Score 34; DB 2; Length 435;
Best Local Similarity 71.4%; Pred. No. 64;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEV 7
Db 303 CRGDETD 309

RESULT 6
JC6507
caspase-2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: JC6507
R;Sato, N.; Milligan, C.E.; Uchiyama, Y.; Oppenheim, R.W.
Gene 202, 127-132, 1997
A;Title: Cloning and expression of the cDNA encoding rat caspase-2.
A;Reference number: JC6507; MUID:98087427; PMID:9427555
A;Accession: JC6507
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-452 <SAT>
A;Cross-references: UNIPROT:O55194; UNIPARC:UPI000000E8A50; GB:U77933; NID:g2769705; PIDN:

Query Match 82.9%; Score 34; DB 2; Length 452;
Best Local Similarity 71.4%; Pred. No. 66;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEV 7
Db 320 CRGDETD 326

RESULT 7
A53305
pentose-5-phosphate 3-epimerase - Rhodospirillum rubrum
C;Species: Rhodospirillum rubrum
C;Date: 08-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 16-Jul-1999
C;Accession: A53305
R;Falcone, D.L.; Tabita, F.R.
J. Bacteriol. 175, 5066-5077, 1993
A;Title: Complementation analysis and regulation of CO-2 fixation gene expression in a ri
A;Reference number: A53305; MUID:93352412; PMID:8349547
A;Accession: A53305
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-219 <FAL>
A;Cross-references: UNIPARC:UPI000016FFB2; GB:S64484; NID:g404535; PIDN:AAE27778.1; PID:g
C;Genetics:
A;Gene: cbbB
C;Superfamily: yeast ribulose-5-phosphate-epimerase

Query Match 80.5%; Score 33; DB 2; Length 219;
Best Local Similarity 71.4%; Pred. No. 53;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEV 7
Db 169 CRGDEVD 175

RESULT 8
F64425

valine-tRNA ligase (EC 6.1.1.9) - Methanococcus jannaschii
 N;Alternate names: valyl-tRNA synthetase
 C;Species: Methanococcus jannaschii
 C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
 C;Accession: F64425
 R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.; Raich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Ison, J.D.; Sadov, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
 Science 273, 1058-1073, 1996
 A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
 A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
 A;Reference number: A64300; MUID:96337999; PMID:8688087
 A;Accession: F64425
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-878 <BUL>
 A;Cross-references: UNIPROT:Q58413; UNIPARC:UPI00001366FC; GB:U67543; GB:L77117; NID:915
 C;Genetics:
 A;Map position: Q08935544-938180
 A;Superfamily: valine-tRNA ligase
 C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 80.5%; Score 33; DB 2; Length 878;
 Best Local Similarity 71.4%; Pred. No. 1.9e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
 | : : : :
 Db 857 CEGEEVD 863

RESULT 9
 H86259
 protein T12C24.14 [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C;Accession: H86259
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Huizar, L.
 Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.; Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: H86259
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-209 <STO>
 A;Cross-references: UNIPROT:Q9LN86; UNIPARC:UPI00000A32FD; GB:AE005172; NID:9502389; PI
 C;Genetics:
 A;Map position: T12C24.14
 A;Superfamily: Arabidopsis thaliana transcription factor DREB1B

Query Match 78.0%; Score 32; DB 2; Length 209;
 Best Local Similarity 71.4%; Pred. No. 79;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
 | : : : :
 Db 128 CAGDDVD 134

RESULT 10
 B96653
 hypothetical protein F16P17.1 [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C;Accession: B96653

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Huizar, L.
 Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.; Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: B96653
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-514 <STO>
 A;Cross-references: UNIPROT:Q9LQ20; UNIPARC:UPI00000AB264; GB:AE005173; NID:98493575; PI
 C;Genetics:
 A;Gene: F16P17.1
 A;Map position: 1

Query Match 78.0%; Score 32; DB 2; Length 514;
 Best Local Similarity 71.4%; Pred. No. 1.8e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
 | : : : :
 Db 312 CKGNKVD 318

RESULT 11
 G72405
 ATP-dependent DNA helicase - Thermotoga maritima (strain MSB8)
 C;Species: Thermotoga maritima
 C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C;Accession: G72405
 R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.N.
 Nature 399, 323-329, 1999
 A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequencing
 A;Reference number: A72200; MUID:99287316; PMID:10360571
 A;Accession: G72405
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-780 <ARN>
 A;Cross-references: UNIPROT:Q9WY48; UNIPARC:UPI00000D3A6F; GB:AE001705; GB:AE0000512; NID:
 A;Experimental source: strain MSB8
 C;Genetics:
 A;Gene: TW0205
 C;Superfamily: DNA helicase recG

Query Match 78.0%; Score 32; DB 2; Length 780;
 Best Local Similarity 71.4%; Pred. No. 2.7e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
 | : : : :
 Db 106 CSGEEVD 112

RESULT 12
 T43638
 caspase-related proteinase 2A (EC 3.4.22.-) - Caenorhabditis elegans
 N;Contains: caspase 2B
 C;Species: Caenorhabditis elegans
 C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
 C;Accession: T43638; T43639
 R;Shaham, S.
 J. Biol. Chem. 273, 35109-35117, 1998
 A;Title: Identification of multiple Caenorhabditis elegans caspases and their potential
 A;Reference number: Z25587; MUID:99074291; PMID:9857046
 A;Accession: T43638
 A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA
A;Residues: 1-826 <SHA>
A;Cross-references: UNIPROT:Q9Y055; UNIPARC:UPI000005606B; EMBL:AF088288; NID:G4063373;
A;Accession: T43639
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 564-826 <SH2>
A;Cross-references: UNIPARC:UPI0000074F3D; EMBL:AF088289; NID:G4063375; PIDN:AAC98296.1;
C;Genetics:
A;Gene: csp-2
A;Map position: 4
C;Keywords: cysteine proteinase; hydrolase

Query Match 78.0%; Score 32; DB 2; Length 826;
Best Local Similarity 57.1%; Pred. No. 2.8e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKGDEVD 7
|:|:|:
Db 700 CRGDRID 706

RESULT 13
S71750
import intermediate-associated 100K protein precursor - garden pea
N;Alternate names: chloroplast inner envelope protein; chloroplastic translocation compo
C;Species: Pisum sativum (garden pea)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 09-Jul-2004
C;Accession: S71750; S78406; JG6116; PC6035
R;Luebeck, J.; Soll, J.; Akita, M.; Nielsen, E.; Keegstra, K.
EMBO J. 15, 4230-4238, 1996
A;Title: Topology of IEPI10, a component of the chloroplastic protein import machinery P
A;Reference number: S71750; MUID:97015123; PMID:8861951
A;Accession: S71750
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-996 <LUE1>
A;Cross-references: UNIPROT:O24293; UNIPARC:UPI00000A0B93; EMBL:Z68506; NID:G1495767; PI
A;Accession: S78406
A;Molecule type: protein
A;Residues: 38-46;537-561;690-697 <LUE2>
A;Cross-references: UNIPARC:UPI00001792E7; UNIPARC:UPI00001792E8; UNIPARC:UPI00001792E9
A;Experimental source: cultivar golf
R;Kessler, F.; Blobel, G.
Proc. Natl. Acad. Sci. U.S.A. 93, 7684-7689, 1996
A;Title: Interaction of the protein import and folding machineries in the chloroplast.
A;Reference number: JG6116; MUID:96353878; PMID:8755536
A;Accession: JG6116
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-312; 'C', 314-358, 'I', 360-363, 'A', 365-415, 'L', 417-593, 'K', 595-661, 'MRITSDTQ
A;Cross-references: UNIPARC:UPI0000095B8; GB:U56419; NID:G1498314; PIDN:AAC49399.1; PI
A;Accession: PC6035
A;Molecule type: protein
A;Residues: 202-222;406-415 'L', 417-425;458-474;706-717;810-822;854-874;961-993 <KES2>
A;Cross-references: UNIPARC:UPI00001792EA; UNIPARC:UPI00001792EB; UNIPARC:UPI00001792EC;
C;Genetics:
A;Genome: nuclear
C;Function:
A;Description: this is an integral membrane protein of the protein import complex of the
C;Superfamily: garden pea import intermediate-associated 100K protein
C;Keywords: chloroplast; inner membrane; transmembrane protein
F;1-37/Domain: transit peptide (chloroplast) #status predicted <TNP>
F;38-996/Product: import intermediate-associated 100K protein #status experimental <MAT>
F;74-93/Domain: transmembrane #status predicted <TM1>
F;101-120/Domain: transmembrane #status predicted <TM2>

Query Match 78.0%; Score 32; DB 2; Length 996;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KGDEVD 7

Db 190 KGDEVD 195
|||||
RESULT 14
S04200
NAD ADP-ribosyltransferase (EC 2.4.2.30) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 31-Dec-2004
C;Accession: S04200
R;Huppi, K.; Bhatia, K.; Siwarski, D.; Klinman, D.; Cherney, B.; Smulson, M.
Nucleic Acids Res. 17, 3387-3401, 1989
A;Title: Sequence and organization of the mouse poly (ADP-ribose) polymerase gene.
A;Reference number: S04200; MUID:89263780; PMID:2498841
A;Accession: S04200
A;Molecule type: DNA
A;Residues: 1-1013 <HUP>
A;Cross-references: UNIPROT:P11103; UNIPARC:UPI000016CBD6; EMBL:X14206; NID:G49893; PIDN:
C;Genetics:
A;Map position: 1
C;Superfamily: poly(ADP-ribose) polymerase
C;Keywords: DNA binding; glycosyltransferase; NAD; nucleus; pentosyltransferase; zinc fir

Query Match 78.0%; Score 32; DB 1; Length 1013;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KGDEVD 7
|||||
Db 209 KGDEVD 214

RESULT 15
A29725
NAD ADP-ribosyltransferase (EC 2.4.2.30), nuclear - human
N;Alternate names: poly (ADP-ribose) polymerase; poly (ADP-ribose) synthetase; poly(ADP)
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 31-Dec-2004
C;Accession: A29725; A28498; A39976; A26901; 138096; B33321; A33321; A35635; A61559; S14(
R;Uchida, K.; Morita, T.; Sato, T.; Ogura, T.; Yamashita, R.; Noguchi, S.; Suzuki, H.; N
Biochem. Biophys. Res. Commun. 148, 617-622, 1987
A;Title: Nucleotide sequence of a full-length cDNA for human fibroblast poly(ADP-ribose)
A;Reference number: A29725; MUID:88076933; PMID:3120710
A;Accession: A29725
A;Molecule type: mRNA
A;Residues: 1-69, 'Q', 71-1014 <UCH>
A;Cross-references: UNIPROT:P09874; UNIPARC:UPI000015E49B; GB:M18112; NID:G190166; PIDN:R;
R;Kurosaki, T.; Ushiro, H.; Mitsuuchi, Y.; Suzuki, S.; Matsuda, M.; Matsuda, Y.; Katunuma
J. Biol. Chem. 262, 15990-15997, 1987
A;Title: Primary structure of human poly (ADP-ribose) synthetase as deduced from cDNA seq
A;Reference number: A28498; MUID:88058958; PMID:2824474
A;Accession: A28498
A;Molecule type: mRNA
A;Residues: 1-16, 'E', 18-211, 'K', 213-236, 'R', 238-366, 'H', 369-1014 <KUR>
A;Cross-references: UNIPARC:UPI0000172437; GB:J03473
R;Cherney, B.W.; McBride, O.W.; Chen, D.; Alkhatib, H.; Bhatia, K.; Hensley, P.; Smulson,
Proc. Natl. Acad. Sci. U.S.A. 84, 8370-8374, 1987
A;Title: cDNA sequence, protein structure, and chromosomal location of the human gene fo
A;Reference number: A39976; MUID:88068596; PMID:2891139
A;Accession: A39976
A;Molecule type: mRNA
A;Residues: 1-49, 'D', 51-612, 'Q', 614-907, 'Y', 909-939, 'R', 941-979, 'I', 981-1014 <CHE>
A;Cross-references: UNIPARC:UPI0000172438; GB:J03030
A;Note: the authors translated the codon ATA for residue 980 as Asn
R;Suzuki, H.; Uchida, K.; Shima, H.; Sato, T.; Okamoto, T.; Kimura, T.; Miwa, M.
Biochem. Biophys. Res. Commun. 146, 403-409, 1987
A;Title: Molecular cloning of cDNA for human poly(ADP-ribose) polymerase and expression c
A;Reference number: A26901; MUID:87298455; PMID:3113420
A;Accession: A26901
A;Molecule type: mRNA
A;Residues: 441-610, 'N', 612-880;921-1014 <SUZ>
A;Cross-references: UNIPARC:UPI0000172439; UNIPARC:UPI000017243A
A;Note: the sequence figure has an omission of forty residues

R; Ogura, T.; Nynuoya, H.; Takahashi-Masutani, M.; Miwa, M.; Sugimura, T.; Esumi, H.
 Biochem. Biophys. Res. Commun. 167, 701-710, 1990
 A; Title: Characterization of a putative promoter region of the human poly(ADP-ribose) polymerase
 A; Reference number: I38096; MUID: 90211250; PMID: 2108670
 A; Accession: I38096
 A; Status: translation not shown
 A; Molecule type: DNA
 A; Residues: 1-40 <RES>
 A; Cross-references: UNIPARC:UPI000016AE52; ENBL:X16674; NID:9510112; PIDN:CAA34663.1; PIDN:CAA34663.1; PIDN:CAA34663.1
 R; Auer, B.; Nagl, U.; Herzog, H.; Schneider, R.; Schweiger, M.
 DNA 8, 575-580, 1989
 A; Title: Human nuclear NAD(+) ADP-ribosyltransferase (polymerizing): organization of the
 A; Reference number: A33321; MUID: 90091744; PMID: 2513174
 A; Accession: B33321
 A; Molecule type: DNA
 A; Residues: 38-43; 93-98; 132-137; 204-209; 237-242; 276-281; 335-340; 384-389; 431-436; 512-517; 517-518; 518-519; 519-520; 520-521; 521-522; 522-523; 523-524; 524-525; 525-526; 526-527; 527-528; 528-529; 529-530; 530-531; 531-532; 532-533; 533-534; 534-535; 535-536; 536-537; 537-538; 538-539; 539-540; 540-541; 541-542; 542-543; 543-544; 544-545; 545-546; 546-547; 547-548; 548-549; 549-550; 550-551; 551-552; 552-553; 553-554; 554-555; 555-556; 556-557; 557-558; 558-559; 559-560; 560-561; 561-562; 562-563; 563-564; 564-565; 565-566; 566-567; 567-568; 568-569; 569-570; 570-571; 571-572; 572-573; 573-574; 574-575; 575-576; 576-577; 577-578; 578-579; 579-580; 580-581; 581-582; 582-583; 583-584; 584-585; 585-586; 586-587; 587-588; 588-589; 589-590; 590-591; 591-592; 592-593; 593-594; 594-595; 595-596; 596-597; 597-598; 598-599; 599-600; 600-601; 601-602; 602-603; 603-604; 604-605; 605-606; 606-607; 607-608; 608-609; 609-610; 610-611; 611-612; 612-613; 613-614; 614-615; 615-616; 616-617; 617-618; 618-619; 619-620; 620-621; 621-622; 622-623; 623-624; 624-625; 625-626; 626-627; 627-628; 628-629; 629-630; 630-631; 631-632; 632-633; 633-634; 634-635; 635-636; 636-637; 637-638; 638-639; 639-640; 640-641; 641-642; 642-643; 643-644; 644-645; 645-646; 646-647; 647-648; 648-649; 649-650; 650-651; 651-652; 652-653; 653-654; 654-655; 655-656; 656-657; 657-658; 658-659; 659-660; 660-661; 661-662; 662-663; 663-664; 664-665; 665-666; 666-667; 667-668; 668-669; 669-670; 670-671; 671-672; 672-673; 673-674; 674-675; 675-676; 676-677; 677-678; 678-679; 679-680; 680-681; 681-682; 682-683; 683-684; 684-685; 685-686; 686-687; 687-688; 688-689; 689-690; 690-691; 691-692; 692-693; 693-694; 694-695; 695-696; 696-697; 697-698; 698-699; 699-700; 700-701; 701-702; 702-703; 703-704; 704-705; 705-706; 706-707; 707-708; 708-709; 709-710; 710-711; 711-712; 712-713; 713-714; 714-715; 715-716; 716-717; 717-718; 718-719; 719-720; 720-721; 721-722; 722-723; 723-724; 724-725; 725-726; 726-727; 727-728; 728-729; 729-730; 730-731; 731-732; 732-733; 733-734; 734-735; 735-736; 736-737; 737-738; 738-739; 739-740; 740-741; 741-742; 742-743; 743-744; 744-745; 745-746; 746-747; 747-748; 748-749; 749-750; 750-751; 751-752; 752-753; 753-754; 754-755; 755-756; 756-757; 757-758; 758-759; 759-760; 760-761; 761-762; 762-763; 763-764; 764-765; 765-766; 766-767; 767-768; 768-769; 769-770; 770-771; 771-772; 772-773; 773-774; 774-775; 775-776; 776-777; 777-778; 778-779; 779-780; 780-781; 781-782; 782-783; 783-784; 784-785; 785-786; 786-787; 787-788; 788-789; 789-790; 790-791; 791-792; 792-793; 793-794; 794-795; 795-796; 796-797; 797-798; 798-799; 799-800; 800-801; 801-802; 802-803; 803-804; 804-805; 805-806; 806-807; 807-808; 808-809; 809-810; 810-811; 811-812; 812-813; 813-814; 814-815; 815-816; 816-817; 817-818; 818-819; 819-820; 820-821; 821-822; 822-823; 823-824; 824-825; 825-826; 826-827; 827-828; 828-829; 829-830; 830-831; 831-832; 832-833; 833-834; 834-835; 835-836; 836-837; 837-838; 838-839; 839-840; 840-841; 841-842; 842-843; 843-844; 844-845; 845-846; 846-847; 847-848; 848-849; 849-850; 850-851; 851-852; 852-853; 853-854; 854-855; 855-856; 856-857; 857-858; 858-859; 859-860; 860-861; 861-862; 862-863; 863-864; 864-865; 865-866; 866-867; 867-868; 868-869; 869-870; 870-871; 871-872; 872-873; 873-874; 874-875; 875-876; 876-877; 877-878; 878-879; 879-880; 880-881; 881-882; 882-883; 883-884; 884-885; 885-886; 886-887; 887-888; 888-889; 889-890; 890-891; 891-892; 892-893; 893-894; 894-895; 895-896; 896-897; 897-898; 898-899; 899-900; 900-901; 901-902; 902-903; 903-904; 904-905; 905-906; 906-907; 907-908; 908-909; 909-910; 910-911; 911-912; 912-913; 913-914; 914-915; 915-916; 916-917; 917-918; 918-919; 919-920; 920-921; 921-922; 922-923; 923-924; 924-925; 925-926; 926-927; 927-928; 928-929; 929-930; 930-931; 931-932; 932-933; 933-934; 934-935; 935-936; 936-937; 937-938; 938-939; 939-940; 940-941; 941-942; 942-943; 943-944; 944-945; 945-946; 946-947; 947-948; 948-949; 949-950; 950-951; 951-952; 952-953; 953-954; 954-955; 955-956; 956-957; 957-958; 958-959; 959-960; 960-961; 961-962; 962-963; 963-964; 964-965; 965-966; 966-967; 967-968; 968-969; 969-970; 970-971; 971-972; 972-973; 973-974; 974-975; 975-976; 976-977; 977-978; 978-979; 979-980; 980-981; 981-982; 982-983; 983-984; 984-985; 985-986; 986-987; 987-988; 988-989; 989-990; 990-991; 991-992; 992-993; 993-994; 994-995; 995-996; 996-997; 997-998; 998-999; 999-1000; 1000-1001; 1001-1002; 1002-1003; 1003-1004; 1004-1005; 1005-1006; 1006-1007; 1007-1008; 1008-1009; 1009-1010; 1010-1011; 1011-1012; 1012-1013; 1013-1014; 1014-1015; 1015-1016; 1016-1017; 1017-1018; 1018-1019; 1019-1020; 1020-1021; 1021-1022; 1022-1023; 1023-1024; 1024-1025; 1025-1026; 1026-1027; 1027-1028; 1028-1029; 1029-1030; 1030-1031; 1031-1032; 1032-1033; 1033-1034; 1034-1035; 1035-1036; 1036-1037; 1037-1038; 1038-1039; 1039-1040; 1040-1041; 1041-1042; 1042-1043; 1043-1044; 1044-1045; 1045-1046; 1046-1047; 1047-1048; 1048-1049; 1049-1050; 1050-1051; 1051-1052; 1052-1053; 1053-1054; 1054-1055; 1055-1056; 1056-1057; 1057-1058; 1058-1059; 1059-1060; 1060-1061; 1061-1062; 1062-1063; 1063-1064; 1064-1065; 1065-1066; 1066-1067; 1067-1068; 1068-1069; 1069-1070; 1070-1071; 1071-1072; 1072-1073; 1073-1074; 1074-1075; 1075-1076; 1076-1077; 1077-1078; 1078-1079; 1079-1080; 1080-1081; 1081-1082; 1082-1083; 1083-1084; 1084-1085; 1085-1086; 1086-1087; 1087-1088; 1088-1089; 1089-1090; 1090-1091; 1091-1092; 1092-1093; 1093-1094; 1094-1095; 1095-1096; 1096-1097; 1097-1098; 1098-1099; 1099-1100; 1100-1101; 1101-1102; 1102-1103; 1103-1104; 1104-1105; 1105-1106; 1106-1107; 1107-1108; 1108-1109; 1109-1110; 1110-1111; 1111-1112; 1112-1113; 1113-1114; 1114-1115; 1115-1116; 1116-1117; 1117-1118; 1118-1119; 1119-1120; 1120-1121; 1121-1122; 1122-1123; 1123-1124; 1124-1125; 1125-1126; 1126-1127; 1127-1128; 1128-1129; 1129-1130; 1130-1131; 1131-1132; 1132-1133; 1133-1134; 1134-1135; 1135-1136; 1136-1137; 1137-1138; 1138-1139; 1139-1140; 1140-1141; 1141-1142; 1142-1143; 1143-1144; 1144-1145; 1145-1146; 1146-1147; 1147-1148; 1148-1149; 1149-1150; 1150-1151; 1151-1152; 1152-1153; 1153-1154; 1154-1155; 1155-1156; 1156-1157; 1157-1158; 1158-1159; 1159-1160; 1160-1161; 1161-1162; 1162-1163; 1163-1164; 1164-1165; 1165-1166; 1166-1167; 1167-1168; 1168-1169; 1169-1170; 1170-1171; 1171-1172; 1172-1173; 1173-1174; 1174-1175; 1175-1176; 1176-1177; 1177-1178; 1178-1179; 1179-1180; 1180-1181; 1181-1182; 1182-1183; 1183-1184; 1184-1185; 1185-1186; 1186-1187; 1187-1188; 1188-1189; 1189-1190; 1190-1191; 1191-1192; 1192-1193; 1193-1194; 1194-1195; 1195-1196; 1196-1197; 1197-1198; 1198-1199; 1199-1200; 1200-1201; 1201-1202; 1202-1203; 1203-1204; 1204-1205; 1205-1206; 1206-1207; 1207-1208; 1208-1209; 1209-1210; 1210-1211; 1211-1212; 1212-1213; 1213-1214; 1214-1215; 1215-1216; 1216-1217; 1217-1218; 1218-1219; 1219-1220; 1220-1221; 1221-1222; 1222-1223; 1223-1224; 1224-1225; 1225-1226; 1226-1227; 1227-1228; 1228-1229; 1229-1230; 1230-1231; 1231-1232; 1232-1233; 1233-1234; 1234-1235; 1235-1236; 1236-1237; 1237-1238; 1238-1239; 1239-1240; 1240-1241; 1241-1242; 1242-1243; 1243-1244; 1244-1245; 1245-1246; 1246-1247; 1247-1248; 1248-1249; 1249-1250; 1250-1251; 1251-1252; 1252-1253; 1253-1254; 1254-1255; 1255-1256; 1256-1257; 1257-1258; 1258-1259; 1259-1260; 1260-1261; 1261-1262; 1262-1263; 1263-1264; 1264-1265; 1265-1266; 1266-1267; 1267-1268; 1268-1269; 1269-1270; 1270-1271; 1271-1272; 1272-1273; 1273-1274; 1274-1275; 1275-1276; 1276-1277; 1277-1278; 1278-1279; 1279-1280; 1280-1281; 1281-1282; 1282-1283; 1283-1284; 1284-1285; 1285-1286; 1286-1287; 1287-1288; 1288-1289; 1289-1290; 1290-1291; 1291-1292; 1292-1293; 1293-1294; 1294-1295; 1295-1296; 1296-1297; 1297-1298; 1298-1299; 1299-1300; 1300-1301; 1301-1302; 1302-1303; 1303-1304; 1304-1305; 1305-1306; 1306-1307; 1307-1308; 1308-1309; 1309-1310; 1310-1311; 1311-1312; 1312-1313; 1313-1314; 1314-1315; 1315-1316; 1316-1317; 1317-1318; 1318-1319; 1319-1320; 1320-1321; 1321-1322; 1322-1323; 1323-1324; 1324-1325; 1325-1326; 1326-1327; 1327-1328; 1328-1329; 1329-1330; 1330-1331; 1331-1332; 1332-1333; 1333-1334; 1334-1335; 1335-1336; 1336-1337; 1337-1338; 1338-1339; 1339-1340; 1340-1341; 1341-1342; 1342-1343; 1343-1344; 1344-1345; 1345-1346; 1346-1347; 1347-1348; 1348-1349; 1349-1350; 1350-1351; 1351-1352; 1352-1353; 1353-1354; 1354-1355; 1355-1356; 1356-1357; 1357-1358; 1358-1359; 1359-1360; 1360-1361; 1361-1362; 1362-1363; 1363-1364; 1364-1365; 1365-1366; 1366-1367; 1367-1368; 1368-1369; 1369-1370; 1370-1371; 1371-1372; 1372-1373; 1373-1374; 1374-1375; 1375-1376; 1376-1377; 1377-1378; 1378-1379; 1379-1380; 1380-1381; 1381-1382; 1382-1383; 1383-1384; 1384-1385; 1385-1386; 1386-1387; 1387-1388; 1388-1389; 1389-1390; 1390-1391; 1391-1392; 1392-1393; 1393-1394; 1394-1395; 1395-1396; 1396-1397; 1397-1398; 1398-1399; 1399-1400; 1400-1401; 1401-1402; 1402-1403; 1403-1404; 1404-1405; 1405-1406; 1406-1407; 1407-1408; 1408-1409; 1409-1410; 1410-1411; 1411-1412; 1412-1413; 1413-1414; 1414-1415; 1415-1416; 1416-1417; 1417-1418; 1418-1419; 1419-1420; 1420-1421; 1421-1422; 1422-1423; 1423-1424; 1424-1425; 1425-1426; 1426-1427; 1427-1428; 1428-1429; 1429-1430; 1430-1431; 1431-1432; 1432-1433; 1433-1434; 1434-1435; 1435-1436; 1436-1437; 1437-1438; 1438-1439; 1439-1440; 1440-1441; 1441-1442; 1442-1443; 1443-1444; 1444-1445; 1445-1446; 1446-1447; 1447-1448; 1448-1449; 1449-1450; 1450-1451; 1451-1452; 1452-1453; 1453-1454; 1454-1455; 1455-1456; 1456-1457; 1457-1458; 1458-1459; 1459-1460; 1460-1461; 1461-1462; 1462-1463; 1463-1464; 1464-1465; 1465-1466; 1466-1467; 1467-1468; 1468-1469; 1469-1470; 1470-1471; 1471-1472; 1472-1473; 1473-1474; 1474-1475; 1475-1476; 1476-1477; 1477-1478; 1478-1479; 1479-1480; 1480-1481; 1481-1482; 1482-1483; 1483-1484; 1484-1485; 1485-1486; 1486-1487; 1487-1488; 1488-1489; 1489-1490; 1490-1491; 1491-1492; 1492-1493; 1493-1494; 1494-1495; 1495-1496; 1496-1497; 1497-1498; 1498-1499; 1499-1500; 1500-1501; 1501-1502; 1502-1503; 1503-1504; 1504-1505; 1505-1506; 1506-1507; 1507-1508; 1508-1509; 1509-1510; 1510-1511; 1511-1512; 1512-1513; 1513-1514; 1514-1515; 1515-1516; 1516-1517; 1517-1518; 1518-1519; 1519-1520; 1520-1521; 1521-1522; 1522-1523; 1523-1524; 1524-1525; 1525-1526; 1526-1527; 1527-1528; 1528-1529; 1529-1530; 1530-1531; 1531-1532; 1532-1533; 1533-1534; 1534-1535; 1535-1536; 1536-1537; 1537-1538; 1538-1539; 1539-1540; 1540-1541; 1541-1542; 1542-1543; 1543-1544; 1544-1545; 1545-1546; 1546-1547; 1547-1548; 1548-1549; 1549-1550; 1550-1551; 1551-1552; 1552-1553; 1553-1554; 1554-1555; 1555-1556; 1556-1557; 1557-1558; 1558-1559; 1559-1560; 1560-1561; 1561-1562; 1562-1563; 1563-1564; 1564-1565; 1565-1566; 1566-1567; 1567-1568; 1568-1569; 1569-1570; 1570-1571; 1571-1572; 1572-1573; 1573-1574; 1574-1575; 1575-1576; 1576-1577; 1577-1578; 1578-1579; 1579-1580; 1580-1581; 1581-1582; 1582-1583; 1583-1584; 1584-1585; 1585-1586; 1586-1587; 1587-1588; 1588-1589; 1589-1590; 1590-1591; 1591-1592; 1592-1593; 1593-1594; 1594-1595; 1595-1596; 1596-1597; 1597-1598; 1598-1599; 1599-1600; 1600-1601; 1601-1602; 1602-1603; 1603-1604; 1604-1605; 1605-1606; 1606-1607; 1607-1608; 1608-1609; 1609-1610; 1610-1611; 1611-1612; 1612-1613; 1613-1614; 1614-1615; 1615-1616; 1616-1617; 1617-1618; 1618-1619; 1619-1620; 1620-1621; 1621-1622; 1622-1623; 1623-1624; 1624-1625; 1625-1626; 1626-1627; 1627-1628; 1628-1629; 1629-1630; 1630-1631; 1631-1632; 1632-1633; 1633-1634; 1634-1635; 1635-1636; 1636-1637; 1637-1638; 1638-1639; 1639-1640; 1640-1641; 1641-1642; 1642-1643; 1643-1644; 1644-1645; 1645-1646; 1646-1647; 1647-1648; 1648-1649; 1649-1650; 1650-1651; 1651-1652; 1652-1653; 1653-1654; 1654-1655; 1655-1656; 1656-1657; 1657-1658; 1658-1659; 1659-1660; 1660-1661; 1661-1662; 1662-1663; 1663-1664; 1664-1665; 1665-1666; 1666-1667; 1667-1668; 1668-1669;

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2005, 11:36:08 ; Search time 170.333 Seconds
(without alignments)
28.994 Million cell updates/sec

Title: US-09-473-619D-2

Perfect score: 41

Sequence: 1 CKGDEVD 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	92.7	248	Q55MS4_CRYNE	Q55m4 cryptococcu
2	38	92.7	248	Q5KB50_CRYNE	Q5kb50 cryptococcu
3	38	92.7	336	Q5LE15_BACFN	Q5le15 bacteroides
4	38	92.7	336	Q64V52_BACFR	Q64v52 bacteroides
5	37	90.2	1070	Q4N1E8_THPA	Q4n1e8 theileria p
6	37	90.2	1104	Q4PAP0_USTMA	Q4pap0 utaligo ma
7	37	90.2	1197	Q4U8P9_THEAN	Q4u8p9 theileria a
8	36	87.8	385	Q8H0F8_COFAR	Q8h0f8 coffea arab
9	36	87.8	385	Q8H0F9_COFAR	Q8h0f9 coffea arab
10	36	87.8	385	Q9AVK1_COFAR	Q9avk1 coffea arab
11	36	87.8	385	Q9AVL9_COFAR	Q9avl9 coffea arab
12	36	87.8	528	Q61RM1_CAEBR	Q61rm1 caenorhabdi
13	36	87.8	589	Q61RL9_CAEBR	Q61rl9 caenorhabdi
14	36	87.8	1230	Q65LJ9_BACLD	Q65lj9 bacillus li
15	35	85.4	275	Q8D9L3_VIBVU	Q8d9l3 vibrio vuln
16	35	85.4	275	Q7MK52_VIBVY	Q7mk52 vibrio vuln
17	35	85.4	278	Q5EBW8_COFCA	Q5ebw8 coffea cane
18	35	85.4	397	Q4SNC6_TETNG	Q4snc6 tetraodon n
19	35	85.4	489	Q5N3V7_SYN6	Q5n3v7 synchococc
20	35	85.4	752	Q7RGK8_PLAYO	Q7rgk8 plasmodium
21	35	85.4	857	Q4Z2Q4_PLABE	Q4z2q4 plasmodium
22	34	82.9	105	Q94GH9_ORYSA	Q94gh9 oryza sativ
23	34	82.9	109	Q4HP49_CAMUP	Q4hp49 campylobact
24	34	82.9	250	Q59UP6_CANAL	Q59up6 candida alb
25	34	82.9	250	Q9HFS1_CANAL	Q9hfs1 candida alb
26	34	82.9	312	CASP2_RAT	P55215 rattus norv
27	34	82.9	352	Q8UCH9_AGR75	Q8uch9 agrobacteri
28	34	82.9	387	Q89Q26_BRAJA	Q89q26 bradyrhizob
29	34	82.9	424	CASP2_CHICK	Q88943 gallus gall
30	34	82.9	435	CASP2_HUMAN	P42575 homo sapien
31	34	82.9	435	CASP2_MOUSE	P29594 mus musculu

32	34	82.9	435	2	Q7KZL6_HUMAN	Q7kzl6 homo sapien
33	34	82.9	438	2	Q4RQC2_TETNG	Q4rqc2 tetraodon n
34	34	82.9	452	2	Q9BUP7_HUMAN	Q9bup7 homo sapien
35	34	82.9	452	2	O55194_RAT	O55194 rattus norv
36	34	82.9	452	2	Q8C9H7_MOUSE	Q8c9h7 mus musculu
37	34	82.9	452	2	Q8K241_MOUSE	Q8k241 mus musculu
38	34	82.9	700	2	O55CN9_DICDI	O55cn9 dictyosteli
39	34	82.9	727	1	YK82_SCHPO	Yk8p4 schizosacch
40	34	82.9	827	2	Q51Q30_MAGGR	Q51q30 magnaporthe
41	33	80.5	154	2	Q7SCV9_NEUCR	Q7scv9 neurospora
42	33	80.5	178	2	O51424_ENTHI	O51424 entamoeba h
43	33	80.5	217	2	Q7P5W8_FUSNV	Q7p5w8 fusobacteri
44	33	80.5	225	1	RPE_RHGRU	P51013 rhodospiril
45	33	80.5	225	2	Q8RLW5_MOUSE	Q8rlw5 mus musculu

ALIGNMENTS

RESULT 1

Q55MS4_CRYNE PRELIMINARY; PRT; 248 AA.

AC Q55MS4;

DT 13-SEP-2005 (TrEMBLrel. 31, Created)

DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

DE Hypothetical protein.

GN ORFNames=CNBH3600;

OS Cryptococcus neoformans var. neoformans B-3501A.

OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;

OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.

OK NCBI_TaxID=283643;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=B-3501A;

RA Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M., Wickes B.L., Fu J., Davis R.W.;

RT "Cryptococcus neoformans serotype D sequencing.";

RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.

CC -!- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.

CC EMBL; AA01000042; EAL19261.1; -; Genomic_DNA.

DR Hypothetical protein.

SQ SEQUENCE 248 AA; 28162 MW; B25C174C91D3A088 CRC64;

Query Match 92.7%; Score 38; DB 2; Length 248;

Best Local Similarity 85.7%; Pred. No. 37;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7

Db 164 CKGDELD 170

RESULT 2

Q5KB50_CRYNE PRELIMINARY; PRT; 248 AA.

AC Q5KB50;

DT 10-MAY-2005 (TrEMBLrel. 30, Created)

DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)

DE Hypothetical protein.

GN ORFNames=CN103770;

OS Cryptococcus neoformans var. neoformans JEC21.

OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;

OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.

OK NCBI_TaxID=214684;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=JEC21;

RA Loftus B., Amedeo P., Roncaglia P., Vanathevan J., Utterback T., Van Aken S., Fraser C.;

```

RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=JBC21;
RX PubMed=1563466; DOI=10.1126/science.1103773;
RA Loftus B.J., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D.,
RA Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,
RA Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,
RA D'Souza C.A., Fox D.S., Grinberg V., Fu J., Fukushima M., Haas B.J.,
RA Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzywinski M.I.,
RA Kwon-Chung K.J., Lengeller K.B., Maiti R., Marra M.A., Marra R.E.,
RA Mathewson C.A., Mitchell T.G., Pertea M., Riggs F.R., Salzberg S.L.,
RA Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A.,
RA Suh B.B., Tenney A., Utterback T.R., Wickes B.L., Wortman J.R.,
RA Wye N.H., Kronstad R.W., Lodge J.K., Heitman J., Davis R.W.,
RA Fraser C.M., Hyman R.W.;
RT "The genome of the basidiomycetous yeast and human pathogen
RL Cryptococcus neoformans."
DR EMBL; AE017349; AAW45282.1; -; Genomic_DNA.
DR InterPro; IPR006384; HAD_Sr_IB_hypl.
DR Pfam; PF06889; Put_PhoPhatase; 1.
DR TIGRFAMs; TIGR01489; DKMTppase-SF; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 248 AA; 28162 MW; B25C174C91D3A088 CRC64;

Query Match 92.7%; Score 38; DB 2; Length 248;
Best Local Similarity 85.7%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKGDEVD 7
Db 164 CKGDELD 170

RESULT 3
Q5LE15_BACFN PRELIMINARY; PRT; 336 AA.
ID Q5LE15_BACFN PRELIMINARY; PRT; 336 AA.
AC Q5LE15;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE Hypothetical protein.
GN OrderedLocusNames=BF1940;
OS Bacteroides fragilis (strain ATCC 25285 / NCTC 9343).
OC Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=272559;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15746427; DOI=10.1126/science.1107008;
RA Cerdeno-Tarraga A.-M., Patrick S., Crossman L.C., Blakely G.,
RA Abratt V., Lennard N., Poxton I., Duerden B., Harris B., Quail M.A.,
RA Barron A., Clark L., Corton C., Doggett J., Holden M.T.G., Larke N.,
RA Line A., Lord A., Norbertzak H., Ormond D., Price C.,
RA Rabinowitz E., Woodward J., Barrell B.G., Parkhill J.;
RT "Extensive DNA inversions in the B. fragilis genome control variable
RT gene expression."
RL Science 307:1463-1465(2005).
DR EMBL; CR626927; CAH07638.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 336 AA; 37916 MW; 43351A58940F3F19 CRC64;

Query Match 92.7%; Score 38; DB 2; Length 336;
Best Local Similarity 85.7%; Pred. No. 49;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKGDEVD 7
Db 227 CRGDEVD 233

RESULT 4
Q5LE15_BACFN PRELIMINARY; PRT; 336 AA.
ID Q5LE15_BACFN PRELIMINARY; PRT; 336 AA.
AC Q5LE15;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE Hypothetical protein.
GN OrderedLocusNames=BF1940;
OS Bacteroides fragilis (strain ATCC 25285 / NCTC 9343).
OC Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=272559;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15746427; DOI=10.1126/science.1107008;
RA Cerdeno-Tarraga A.-M., Patrick S., Crossman L.C., Blakely G.,
RA Abratt V., Lennard N., Poxton I., Duerden B., Harris B., Quail M.A.,
RA Barron A., Clark L., Corton C., Doggett J., Holden M.T.G., Larke N.,
RA Line A., Lord A., Norbertzak H., Ormond D., Price C.,
RA Rabinowitz E., Woodward J., Barrell B.G., Parkhill J.;
RT "Extensive DNA inversions in the B. fragilis genome control variable
RT gene expression."
RL Science 307:1463-1465(2005).
DR EMBL; CR626927; CAH07638.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 336 AA; 37916 MW; 43351A58940F3F19 CRC64;

Query Match 92.7%; Score 38; DB 2; Length 336;
Best Local Similarity 85.7%; Pred. No. 49;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKGDEVD 7
Db 227 CRGDEVD 233

RESULT 5
Q4N1E8_THEPA PRELIMINARY; PRT; 1070 AA.
ID Q4N1E8_THEPA PRELIMINARY; PRT; 1070 AA.
AC Q4N1E8;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Hypothetical protein.
GN ORFNames=TP04_0796;
OS Theileria parva.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
OC Theileria.
OX NCBI_TaxID=5875;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Muguga;
RA Gardner M.J., Bishop R., Shah T., de Villiers E.P., Carlton J.M.,
RA Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M.,
RA Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J.,
RA Jiang L., Lynn J., Weaver B., Shoaibi A., Wasawo D., Crabtree J.,
RA Wortman J.R., Haas B., Angiulli S.V., Creasy T.H., Lu C., Suh B.,
RA Silva J.C., Utterback T.R., Feldblyum T.V., Pertea M., Allen J.,
RA Taracha E.L.N., Salzberg S.L., White O.R., Fitzhugh H.A., Morzaria S.,
RA Venter J.C., Fraser C.M., Nene V.;
RT "Genome sequence of Theileria parva, a bovine pathogen that transforms
RT lymphocytes."
RL Science 309:134-137(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Muguga;
RA Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N.,
RA Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,
RA Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J., Jiang L.,
RA Lynn J., Weaver B., Shoaibi A., Wasawo D., Crabtree J., Wortman J.R.,
RA Haas B., Angiulli S., Creasy T.H., Lu C., Suh B., Silva J.C.,
RA Utterback T., Feldblyum T., Pertea M., Allen J., Taracha E.L.,
RA Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,
RA Fraser C.M., Nene V.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.

```

```

Q64V52_BACFR PRELIMINARY; PRT; 336 AA.
ID Q64V52;
AC Q64V52;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Putative periplasmic protein.
GN OrderedLocusNames=BF1878;
OS Bacteroides fragilis.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=817;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=YCH46;
RX PubMed=15466707; DOI=10.1073/pnas.0404172101;
RA Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
RA Kuhara S., Yattori M., Hayashi T., Ohnishi Y.;
RT "Genomic analysis of Bacteroides fragilis reveals extensive DNA
RT inversions regulating cell surface adaptation."
DR Proc. Natl. Acad. Sci. U.S.A. 101:14919-14924(2004).
RL EMBL; AP006841; BAD48626.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 336 AA; 37915 MW; 47D554589759D119 CRC64;

Query Match 92.7%; Score 38; DB 2; Length 336;
Best Local Similarity 85.7%; Pred. No. 49;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKGDEVD 7
Db 227 CRGDEVD 233

RESULT 5
Q4N1E8_THEPA PRELIMINARY; PRT; 1070 AA.
ID Q4N1E8_THEPA PRELIMINARY; PRT; 1070 AA.
AC Q4N1E8;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Hypothetical protein.
GN ORFNames=TP04_0796;
OS Theileria parva.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
OC Theileria.
OX NCBI_TaxID=5875;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Muguga;
RA Gardner M.J., Bishop R., Shah T., de Villiers E.P., Carlton J.M.,
RA Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M.,
RA Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J.,
RA Jiang L., Lynn J., Weaver B., Shoaibi A., Wasawo D., Crabtree J.,
RA Wortman J.R., Haas B., Angiulli S.V., Creasy T.H., Lu C., Suh B.,
RA Silva J.C., Utterback T.R., Feldblyum T.V., Pertea M., Allen J.,
RA Taracha E.L.N., Salzberg S.L., White O.R., Fitzhugh H.A., Morzaria S.,
RA Venter J.C., Fraser C.M., Nene V.;
RT "Genome sequence of Theileria parva, a bovine pathogen that transforms
RT lymphocytes."
RL Science 309:134-137(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Muguga;
RA Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N.,
RA Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,
RA Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J., Jiang L.,
RA Lynn J., Weaver B., Shoaibi A., Wasawo D., Crabtree J., Wortman J.R.,
RA Haas B., Angiulli S., Creasy T.H., Lu C., Suh B., Silva J.C.,
RA Utterback T., Feldblyum T., Pertea M., Allen J., Taracha E.L.,
RA Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,
RA Fraser C.M., Nene V.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.

```


CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAGK01000004; EAN32150.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 1070 AA; 117312 MW; F04666F536FBE05F CRC64;

Query Match 90.2%; Score 37; DB 2; Length 1070;
 Best Local Similarity 85.7%; Pred. No. 2.4e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
 |||||
 Db 386 CKGDETD 392

RESULT 6

Q4PAP0_USTWA PRELIMINARY; PRT; 1104 AA.
 AC Q4PAP0;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=OM02823.1;
 OS Ustilago maydis 521.
 OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
 OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
 OX NCBI_TaxID=237631;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=521;
 RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
 RA Ait-zahra M., Allen T., An P., Anderson M., Anderson S.,
 RA Atchachi H., Ambruster J., Bachantaeng P., Baldwin J., Barry A.,
 RA Bayul T., Blitshteyn B., Bloom T., Blye J., Boguelavskiy L.,
 RA Borowsky M., Boukhgalter B., Brunache A., Butier J., Calixte N.,
 RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
 RA Collimore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
 RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
 RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
 RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
 RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,
 RA Girke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
 RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
 RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
 RA Jaffe D., Jones C., Kanal M., Kanat A., Kamvaselis M., Karlsson E.,
 RA Kells C., Kieu A., Kiser P., Kodira C., Kulbokas E., Labutti K.,
 RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
 RA Lindblad-toh K., Liu X., Lokyitsang T., Lokyitsang Y., Lucien O.,
 RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
 RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,
 RA McCarthy M., McDonough S., Mcghee T., Meldrim J., Meneus L.,
 RA Mesirov J., Mihalev A., Minova T., Mikkelsen T., Mlenga V., Moru K.,
 RA Mozes J., Mulrain L., Munson G., Naylor J., News C., Nguyen C.,
 RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
 RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotosho B.,
 RA O'Neill K., Osman S., Parker S., Perrin D., Phunkhang P., Piquani B.,
 RA Purcell S., Rachupka T., Ramaamy U., Rameau R., Ray V., Raymond C.,
 RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
 RA Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,
 RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnuez C.,
 RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
 RA Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
 RA Tenzing P., Tesfaye S., Theodore J., Thoultsang Y., Topham K.,
 RA Towey S., Tsamila T., Tsomo N., Vallee D., Vassiliev H.,
 RA Venkataranan V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
 RA Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
 RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
 RA Zimmer A., Zody M., Lander E.
 RT "The genome sequence of Ustilago maydis."
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AACP01000096; EAK83869.1; -; Genomic_DNA.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR003959; AAA_ATPase_cent.
 DR InterPro; IPR000862; RFC.
 DR Pfam; PF00004; AAA; 1.
 DR SMART; SM00382; AAA; 1.
 KW ATP-binding; Hypothetical protein; Nucleotide-binding.
 SQ SEQUENCE 1104 AA; 121289 MW; 56A22E41A3C0C25 CRC64;

Query Match 90.2%; Score 37; DB 2; Length 1104;
 Best Local Similarity 85.7%; Pred. No. 2.4e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
 |||||
 Db 982 CKGDKVD 988

RESULT 7

Q4U8P9_THEAN PRELIMINARY; PRT; 1197 AA.
 AC Q4U8P9;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=TA09935;
 OS Theileria annulata.
 OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;
 OC Theileria.
 OX NCBI_TaxID=5874;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Ankara isolate clone C9;
 RA Pain A., Renaud H., Murphy L., Harris D.A., Quail M.A., Berriman M.,
 RA Hall N., Barrell B.G.;
 RT "The chromosome 3 genome sequence of Theileria annulata."
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR940353; CAI76804.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 1197 AA; 132105 MW; E613399C9F4B1856 CRC64;

Query Match 90.2%; Score 37; DB 2; Length 1197;
 Best Local Similarity 85.7%; Pred. No. 2.6e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
 |||||
 Db 484 CKGDETD 490

RESULT 8

Q8H0F8_COPAR PRELIMINARY; PRT; 385 AA.
 AC Q8H0F8;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Tentative caffeine synthase 4.
 GN Name=CtCS4;
 OS Coffea arabica (Coffee).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC lamiales; Gentianales; Rubiaceae; Ixoroideae; Coffeae; Coffea.
 OX NCBI_TaxID=13443;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RL MEDLINE=22415056; PubMed=12527364; DOI=10.1016/S0014-5793(02)03781-X;
 RA Mizuno K., Okuda A., Kato M., Yoneyama N., Tanaka H., Ashihara H.,
 RA Fujimura T.;
 RT "Isolation of a new dual-functional caffeine synthase gene encoding an

RT enzyme for the conversion of 7-methylxanthine to caffeine from coffee
RT (Coffea arabica L.), -;
RL FBBS Lett. 534:75-81(2003).
DR EMBL; AB054843; BAC43759.1; -; mRNA.
DR HSP; Q9SPV4; 1M6E.
DR InterPro; IPR005299; Methyltransf 6.
DR Pfam; PF03492; Methyltransf 7; 1.
SQ SEQUENCE 385 AA; 43270 MW; 26E5858349DB0DD6 CRC64;

Query Match 87.8%; Score 36; DB 2; Length 385;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
| | | | |
Db 228 CKGDECD 234

RESULT 9

Q8HOF9_COFAR
ID Q8HOF9_COFAR PRELIMINARY; PRT; 385 AA.
AC Q8HOF9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 23, Last annotation update)
DE Tentative caffeine synthase 3.
GN Name=CtCS3;
GN Name=CtCS3;
OS Coffea arabica (Coffee).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Gentianales; Rubiaceae; Ixoroideae; Coffeae; Coffea.
OX NCBI_TaxID=13443;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22415056; PubMed=12527364; DOI=10.1016/S0014-5793(02)03781-X;
RA Mizuno K., Okuda A., Kato M., Yoneyama N., Tanaka H., Ashihara H.,
RA Fujimura T.;
RT "Isolation of a new dual-functional caffeine synthase gene encoding an
RT enzyme for the conversion of 7-methylxanthine to caffeine from coffee
RT (Coffea arabica L.).";
RL FBBS Lett. 534:75-81(2003).
DR EMBL; AB054842; BAC43758.1; -; mRNA.
DR HSP; Q9SPV4; 1M6E.
DR InterPro; IPR005299; Methyltransf 6.
DR Pfam; PF03492; Methyltransf 7; 1.
SQ SEQUENCE 385 AA; 43221 MW; 84942A3FB806F301 CRC64;

Query Match 87.8%; Score 36; DB 2; Length 385;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
| | | | |
Db 228 CKGDECD 234

RESULT 10

Q9AVK1_COFAR
ID Q9AVK1_COFAR PRELIMINARY; PRT; 385 AA.
AC Q9AVK1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Theobromine synthase.
GN Name=CaMTL2;
GN Name=CaMTL2;
OS Coffea arabica (Coffee).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Gentianales; Rubiaceae; Ixoroideae; Coffeae; Coffea.
OX NCBI_TaxID=13443;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21269383; PubMed=11108716; DOI=10.1074/jbc.M009480200;

RA Ogawa M., Herai Y., Koizumi N., Kusano T., Sano H.;
RT "7-Methylxanthine methyltransferase of coffee plants. Gene isolation
RT and enzymatic properties.";
RL J. Biol. Chem. 276:8213-8218(2001).
DR EMBL; AB048792; BAB39214.1; -; mRNA.
DR HSP; Q9SPV4; 1M6E.
DR InterPro; IPR005299; Methyltransf 6.
DR Pfam; PF03492; Methyltransf 7; 1.
SQ SEQUENCE 385 AA; 43270 MW; 92103A20A001FB0E CRC64;

Query Match 87.8%; Score 36; DB 2; Length 385;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
| | | | |
Db 228 CKGDECD 234

RESULT 11

Q9AVL9_COFAR
ID Q9AVL9_COFAR PRELIMINARY; PRT; 385 AA.
AC Q9AVL9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Caffeine synthase.
GN Name=CaMTL1;
OS Coffea arabica (Coffee).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Gentianales; Rubiaceae; Ixoroideae; Coffeae; Coffea.
OX NCBI_TaxID=13443;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Callus;
RX MEDLINE=21269383; PubMed=11108716; DOI=10.1074/jbc.M009480200;

RA Ogawa M., Herai Y., Koizumi N., Kusano T., Sano H.;
RT "7-Methylxanthine methyltransferase of coffee plants. Gene isolation
RT and enzymatic properties.";
RL J. Biol. Chem. 276:8213-8218(2001).
DR EMBL; AB039725; BAB39213.1; -; mRNA.
DR HSP; Q9SPV4; 1M6E.
DR InterPro; IPR005299; Methyltransf 6.
DR Pfam; PF03492; Methyltransf 7; 1.
SQ SEQUENCE 385 AA; 43242 MW; 003A5837FF0AE300 CRC64;

Query Match 87.8%; Score 36; DB 2; Length 385;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
| | | | |
Db 228 CKGDECD 234

RESULT 12

Q6IRMI_CAEBR
ID Q6IRMI_CAEBR PRELIMINARY; PRT; 528 AA.
AC Q6IRMI;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein CBG06533.
GN Name=CBG06533;
GN Name=CBG06533;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RG The C.Briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.

CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAAC01000029; CAB62441.1; -; Genomic_DNA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005006; F:epidermal growth factor receptor activity; IEA.
 DR InterPro; IPR000494; EGFR_L.
 DR Pfam; PF01030; Recep_L_domain; 3.
 KW Hypothetical protein.
 SQ SEQUENCE 528 AA; 61142 MW; F88CFE2098876A6D CRC64;

Query Match 87.8%; Score 36; DB 2; Length 528;
 Best Local Similarity 71.4%; Pred. No. 1.9e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
 Db 189 CQGDEID 195
 |||||

RESULT 13

Q61RL9 CAEBR
 ID Q61RL9 CAEBR PRELIMINARY; PRT; 589 AA.
 AC Q61RL9
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein CBG06535.
 DN Name=CBG06535;
 OS Caenorhabditis briggsae.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6238;
 RN [1]

NUCLEOTIDE SEQUENCE

RP The C.briggsae Sequencing Consortium;
 RG Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 RL -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAAC01000029; CAB62443.1; -; Genomic_DNA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005006; F:epidermal growth factor receptor activity; IEA.
 DR InterPro; IPR000494; EGFR_L.
 DR Pfam; PF01030; Recep_L_domain; 2.
 KW Hypothetical protein.
 SQ SEQUENCE 589 AA; 67033 MW; 62B886BB3A7FC579 CRC64;

Query Match 87.8%; Score 36; DB 2; Length 589;
 Best Local Similarity 71.4%; Pred. No. 2.1e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
 Db 102 CQGDEID 108
 |||||

RESULT 14

Q65LJ9 BACLD
 ID Q65LJ9 BACLD PRELIMINARY; PRT; 1230 AA.
 AC Q65LJ9; Q62W20;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Adda (ATP-dependent deoxyribonuclease) (Subunit A).
 GN Name=adda; OrderedLocNames=BL01350, BL01157;
 OS Bacillus licheniformis (strain DSM 13 / ATCC 14580).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=279010;
 RN [1]

NUCLEOTIDE SEQUENCE

RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15383718; DOI=10.1159/000079829;
 RA Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,

RA Ehrenreich P., Baumer S., Henne A., Liesegang H., Merkl R.,
 RA Ehrenreich A., Gottschalk G.;
 RT "The complete genome sequence of *Bacillus licheniformis* DSM13, an
 RT organism with great industrial potential.";
 RL J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15461803; DOI=10.1186/gb-2004-5-10-r77;
 RA Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J.,
 RA Tang M., Lopez de Leon A., Xiang H., Gusti V., Clausen I.G.,
 RA Olsen P.B., Rasmussen M.D., Andersen J.T., Joergensen P.L.,
 RA Larsen T.S., Sorokin A., Bolotin A., Lapidus A., Galleron N.,
 RA Ehrlich S.D., Berka R.M.;
 RT "Complete genome sequence of the industrial bacterium *Bacillus*
 RT *licheniformis* and comparisons with closely related *Bacillus* species.";
 RL Genome Biol. 5:RESEARCH077.1-RESEARCH077.12(2004).
 DR EMBL; AE017333; AAU40065.1; -; Genomic_DNA.
 DR EMBL; CP000002; AAU22718.1; -; Genomic_DNA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004003; F:ATP-dependent DNA helicase activity; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0006281; F:DNA repair; IEA.
 DR InterPro; IPR00212; UvrD-helicase.
 DR Pfam; PF00580; UvrD-helicase; 1.
 KW Complete proteome.
 SQ SEQUENCE 1230 AA; 141091 MW; 10DDC24F1AC42C2F CRC64;

Query Match 87.8%; Score 36; DB 2; Length 1230;
 Best Local Similarity 85.7%; Pred. No. 4.3e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
 Db 292 CKGDEVD 298
 |||||

RESULT 15

Q8D9L3 VIBVU
 ID Q8D9L3 VIBVU PRELIMINARY; PRT; 275 AA.
 AC Q8D9L3;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Uncharacterized protein required for formate dehydrogenase
 DE activity.
 GN OrderedLocNames=VV12584;
 OS *Vibrio vulnificus*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; *Vibrio*.
 OX NCBI_TaxID=672;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CMCP6;
 RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
 RA Choy H.E.;
 RT "Complete genome sequence of *Vibrio vulnificus* CMCP6.";
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE016805; AA010935.1; -; Genomic_DNA.
 DR GO; GO:0009326; C:formate dehydrogenase complex; IEA.
 DR GO; GO:0008863; F:formate dehydrogenase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR003786; FdhD.
 DR Pfam; PF02634; FdhD-NarQ; 1.
 DR PIRSF; PIRSF015626; FdhD; 1.
 KW Complete proteome.
 SQ SEQUENCE 275 AA; 30510 MW; 4C09A7F76FEBDB25 CRC64;

Query Match 85.4%; Score 35; DB 2; Length 275;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CKGDEVD 6
 |||||

Db 168 CKGDEV 173

Search completed: December 27, 2005, 11:48:19
Job time : 173.333 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2005, 11:36:08 ; Search time 37.9167 Seconds
(without alignments)
15.263 Million cell updates/sec

Title: US-09-473-619D-2

Perfect score: 41

Sequence: 1 CKGDEVD 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA.*

- 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	87.8	385	2	US-09-971-020A-3
2	36	87.8	385	2	US-09-971-020A-5
3	34	82.9	56	2	US-09-187-789-58
4	34	82.9	56	2	US-09-139-600-53
5	34	82.9	56	2	US-09-989-903-58
6	34	82.9	92	2	US-09-902-540-14307
7	34	82.9	251	2	US-09-248-796A-23216
8	34	82.9	421	2	US-08-983-502-10
9	34	82.9	421	2	US-09-516-747-10
10	34	82.9	421	4	PCT-US96-10521-10
11	34	82.9	435	2	US-08-258-287B-53
12	34	82.9	435	2	US-08-368-704C-51
13	34	82.9	435	2	US-09-561-756-9
14	34	82.9	435	2	US-09-227-721-9
15	34	82.9	435	2	US-08-816-075-2
16	34	82.9	435	2	US-08-724-378D-9
17	34	82.9	435	2	US-09-954-697-9
18	34	82.9	435	2	US-09-291-289-10
19	34	82.9	435	2	US-09-851-873-97
20	34	82.9	435	4	PCT-US94-07127A-4
21	34	82.9	441	2	US-08-258-287B-44
22	34	82.9	441	2	US-08-368-704C-43
23	34	82.9	451	2	US-09-888-243-28
24	33	80.5	267	2	US-10-104-047-3902
25	33	80.5	423	2	US-09-252-991A-31821
26	32	78.0	7	1	US-08-421-702A-8
27	32	78.0	7	1	US-08-421-696A-8

28	32	78.0	7	1	US-08-421-697A-8	Sequence 8, Appli
29	32	78.0	7	1	US-08-421-698A-8	Sequence 8, Appli
30	32	78.0	7	1	US-08-421-695A-8	Sequence 8, Appli
31	32	78.0	7	4	PCT-US95-04741-8	Sequence 27, Appl
32	32	78.0	9	1	US-08-421-702A-27	Sequence 27, Appl
33	32	78.0	9	1	US-08-421-696A-27	Sequence 27, Appl
34	32	78.0	9	1	US-08-421-697A-27	Sequence 27, Appl
35	32	78.0	9	1	US-08-421-698A-27	Sequence 27, Appl
36	32	78.0	9	1	US-08-421-695A-27	Sequence 27, Appl
37	32	78.0	9	4	PCT-US95-04741-27	Sequence 60, Appl
38	32	78.0	15	2	US-08-789-333F-60	Sequence 60, Appl
39	32	78.0	15	2	US-08-787-738B-60	Sequence 60, Appl
40	32	78.0	15	2	US-09-916-940-60	Sequence 60, Appl
41	32	78.0	15	2	US-10-096-550-60	Sequence 23, Appl
42	32	78.0	26	2	US-09-302-812-23	Sequence 24, Appl
43	32	78.0	26	2	US-09-302-812-24	Sequence 25, Appl
44	32	78.0	26	2	US-09-302-812-25	Sequence 23, Appl
45	32	78.0	26	2	US-09-511-477-23	

ALIGNMENTS

RESULT 1

US-09-971-020A-3
; Sequence 3, Application US/09971020A
; Patent No. 6734342
; GENERAL INFORMATION:
; APPLICANT: Sano, Hiroshi
; APPLICANT: Kusano, Tomonobu
; APPLICANT: Koizumi, No. 6734342omu
; TITLE OF INVENTION: Theobromine Synthase Polypeptide of Coffee Plant and the
; TITLE OF INVENTION: Gene Encoding Said Polypeptide
; FILE REFERENCE: 026350-068
; CURRENT APPLICATION NUMBER: US/09/971,020A
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: JP 2000-307,149
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Coffea arabica
US-09-971-020A-3

Query Match 87.8%; Score 16; DB 2; Length 385;
Best Local Similarity 85.7%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CKGDEVD 7
Db 228 CKGDECD 234

RESULT 2

US-09-971-020A-5
; Sequence 5, Application US/09971020A
; Patent No. 6734342
; GENERAL INFORMATION:
; APPLICANT: Sano, Hiroshi
; APPLICANT: Kusano, Tomonobu
; APPLICANT: Koizumi, No. 6734342omu
; TITLE OF INVENTION: Theobromine Synthase Polypeptide of Coffee Plant and the
; TITLE OF INVENTION: Gene Encoding Said Polypeptide
; FILE REFERENCE: 026350-068
; CURRENT APPLICATION NUMBER: US/09/971,020A
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: JP 2000-307,149
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5

```
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Coffea arabica
US-09-971-020A-5

Query Match      87.8%; Score 36; DB 2; Length 385;
Best Local Similarity 85.7%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
Db 228 CKGDEFD 234

RESULT 3
US-09-187-789-58
; Sequence 58, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-187-789-58

Query Match      82.9%; Score 34; DB 2; Length 56;
Best Local Similarity 71.4%; Pred. No. 26;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
Db 31 CRGDETD 37

RESULT 4
US-09-139-600-53
; Sequence 53, Application US/09139600
; Patent No. 6432628
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434
; CURRENT APPLICATION NUMBER: US/09/139,600
; CURRENT FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-139-600-53

Query Match      82.9%; Score 34; DB 2; Length 56;
Best Local Similarity 71.4%; Pred. No. 26;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
Db 31 CRGDETD 37

RESULT 5
```

```
US-09-989-903-58
; Sequence 58, Application US/09989903
; Patent No. 6797812
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434D1
; CURRENT APPLICATION NUMBER: US/09/989,903
; CURRENT FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-989-903-58

Query Match      82.9%; Score 34; DB 2; Length 56;
Best Local Similarity 71.4%; Pred. No. 26;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
Db 31 CRGDETD 37

RESULT 6
US-09-902-540-14307
; Sequence 14307, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 14307
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-14307

Query Match      82.9%; Score 34; DB 2; Length 92;
Best Local Similarity 71.4%; Pred. No. 41;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
Db 68 CKGDAD 74

RESULT 7
US-09-248-796A-23216
; Sequence 23216, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
```

; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 23216
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-23216

Query Match 82.9%; Score 34; DB 2; Length 251;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
 | | | | |
Db 95 CKGKEVD 101

RESULT 8
US-08-983-502-10
; Sequence 10, Application US/08983502
; Patent No. 639327
; GENERAL INFORMATION:
; APPLICANT: David WALLACH
; APPLICANT: Mark P. BOLDIN
; APPLICANT: Tanya M. GONCHAROV
; APPLICANT: Yuriy V. GOLTSEV
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
; TITLE OF INVENTION: AND OTHER PROTEINS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,502
FILING DATE: 16-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10521
FILING DATE: 14-JUN-1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114,615
FILING DATE: 16-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114,986
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 115,319
FILING DATE: 14-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 116,588
FILING DATE: 27-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 117,932
FILING DATE: 16-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH=19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
TYPE: amino acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-983-502-10

Query Match 82.9%; Score 34; DB 2; Length 421;
Best Local Similarity 71.4%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
 | : | | | |
Db 289 CRGDETD 295

RESULT 9
US-09-516-747-10
; Sequence 10, Application US/09516747
; Patent No. 6586571
; GENERAL INFORMATION:
; APPLICANT: David WALLACH
; APPLICANT: Mark P. BOLDIN
; APPLICANT: Tanya M. GONCHAROV
; APPLICANT: Yuriy V. GOLTSEV
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
; TITLE OF INVENTION: AND OTHER PROTEINS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,747
FILING DATE: 01-Mar-2000

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/983,502
FILING DATE: <Unknown>
APPLICATION NUMBER: IL 114,615
FILING DATE: 16-JUL-1995
APPLICATION NUMBER: IL 114,986
FILING DATE: 17-AUG-1995
APPLICATION NUMBER: IL 115,319
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: IL 116,588
FILING DATE: 27-DEC-1995
APPLICATION NUMBER: IL 117,932
FILING DATE: 16-APR-1996

ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH=19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-09-516-747-10

Query Match 82.9%; Score 34; DB 2; Length 421;
Best Local Similarity 71.4%; Pred. No. 1.7e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
Db 289 CRGDETD 295

RESULT 10
PCT-US96-10521-10
; Sequence 10, Application PC/TUS96/10521
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
; TITLE OF INVENTION: AND OTHER PROTEINS
; NUMBER OF SEQUENCES: 34
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10521
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 114,615
; FILING DATE: 16-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 114,986
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 115,319
; FILING DATE: 14-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 116,588
; FILING DATE: 27-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 117,932
; FILING DATE: 16-APR-1996
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 421 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-10521-10

Query Match 82.9%; Score 34; DB 4; Length 421;
Best Local Similarity 71.4%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
Db 289 CRGDETD 295

RESULT 11
US-08-258-287B-53
; Sequence 53, Application US/08258287B
; Patent No. 6083735
; GENERAL INFORMATION:
; APPLICANT: Yuan, Junying
; TITLE OF INVENTION: Programmed Cell Death Genes and Proteins
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005

Query Match 82.9%; Score 34; DB 2; Length 435;
Best Local Similarity 71.4%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
Db 303 CRGDETD 309

RESULT 12
US-08-368-704C-51
; Sequence 51, Application US/08368704C
; Patent No. 6087160
; GENERAL INFORMATION:
; APPLICANT: Yuan, Junying
; APPLICANT: Miura, Masayuki
; TITLE OF INVENTION: Programmed Cell Death Genes and Proteins
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/368,704C
; FILING DATE: 4-JAN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/258,287
; FILING DATE: 10-JUN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/080,850
; FILING DATE: 24-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bugaisky, Lawrence B.
; REGISTRATION NUMBER: 35,086
; REFERENCE/DOCKET NUMBER: 0609.3920002

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
TELEX: 248636 SSK
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-368-704C-51

Query Match 82.9%; Score 34; DB 2; Length 435;
Best Local Similarity 71.4%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
|:|||||
Db 303 CRGDETD 309

RESULT 13
US-09-561-756-9
; Sequence 9, Application US/09561756
; Patent No. 6376226
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
; FILE REFERENCE: 480140.431
; CURRENT APPLICATION NUMBER: US/09/561.756
; CURRENT FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 09/227,721
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-561-756-9

Query Match 82.9%; Score 34; DB 2; Length 435;
Best Local Similarity 71.4%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
|:|||||
Db 303 CRGDETD 309

RESULT 14
US-09-227-721-9
; Sequence 9, Application US/09227721
; Patent No. 6379950
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
; FILE REFERENCE: 480140.431
; CURRENT APPLICATION NUMBER: US/09/227.721
; CURRENT FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-227-721-9

Query Match 82.9%; Score 34; DB 2; Length 435;
Best Local Similarity 71.4%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
|:|||||
Db 303 CRGDETD 309

RESULT 15
US-08-816-075-2
; Sequence 2, Application US/08816075
; Patent No. 6416753
; GENERAL INFORMATION:
; APPLICANT: Yuan, Junying
; APPLICANT: Friedlander, Robert
; TITLE OF INVENTION: Programmed Cell Death and Interleukin-1
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,075
; FILING DATE: 13-MAR-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,524
; FILING DATE: 15-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bugaisky, Lawrence B.
; REGISTRATION NUMBER: 35,086
; REFERENCE/DOCKET NUMBER: 0609.421001/JAG/LBB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 435 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-816-075-2

Query Match 82.9%; Score 34; DB 2; Length 435;
Best Local Similarity 71.4%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
|:|||||
Db 303 CRGDETD 309

Search completed: December 27, 2005, 11:38:42
Job time : 37.9167 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2005, 11:37:12 ; Search time 129.5 Seconds
(without alignments)
22.585 Million cell updates/sec

Title: US-09-473-619D-2

Perfect score: 41

Sequence: 1 CKGDEVD 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	90.2	72	4	US-10-767-701-54704
2	37	90.2	102	4	US-10-425-115-357468
3	37	90.2	103	4	US-10-425-114-68057
4	36	87.8	385	3	US-09-971-020-3
5	36	87.8	385	3	US-09-971-020-3
6	36	87.8	385	4	US-10-802-773-3
7	36	87.8	385	4	US-10-802-773-5
8	36	87.8	385	5	US-10-732-923-10503
9	36	87.8	385	5	US-10-732-923-10504
10	36	87.8	385	5	US-10-732-923-10505
11	36	87.8	385	5	US-10-732-923-10506
12	35	85.4	51	4	US-10-424-599-257727
13	35	85.4	103	4	US-10-767-701-57012
14	35	85.4	393	4	US-10-425-115-330473
15	35	85.4	521	4	US-10-424-599-193383
16	34	82.9	56	3	US-09-989-903-58
17	34	82.9	56	4	US-10-068-564-58
18	34	82.9	56	5	US-10-870-765-58
19	34	82.9	105	4	US-10-437-963-103838
20	34	82.9	283	6	US-11-021-951-169
21	34	82.9	397	4	US-10-424-599-241939
22	34	82.9	421	4	US-10-368-438-10
23	34	82.9	435	2	US-08-459-455-51
24	34	82.9	435	3	US-09-954-637-9
25	34	82.9	435	3	US-03-851-873-97
26	34	82.9	435	4	US-10-280-670-9
27	34	82.9	435	5	US-10-973-858-16

ALIGNMENTS

RESULT 1

US-10-767-701-54704
; Sequence 54704, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 54704
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 14592790.pep
US-10-767-701-54704

Query Match 90.2%; Score 37; DB 4; Length 72;
Best Local Similarity 71.4%; Pred. No. 31;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
Db 38 CRGDEID 44
|:|:|:|:
|:|:|:|:

RESULT 2

US-10-425-115-357468
; Sequence 357468, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10767,701
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 357468
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Zea mays

; FEATURE:
; OTHER INFORMATION: Clone ID: MFT4577_89180C.1.pep
US-10-425-115-357468

Query Match 90.2%; Score 37; DB 4; Length 102;
Best Local Similarity 71.4%; Pred. No. 44;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
|:||||:|
Db 66 CRGDEID 72

RESULT 3
US-10-425-114-68057
; Sequence 68057, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 68057
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73019E09_FLI.pep
US-10-425-114-68057

Query Match 90.2%; Score 37; DB 4; Length 103;
Best Local Similarity 71.4%; Pred. No. 44;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
|:||||:|
Db 66 CRGDEID 72

RESULT 4
US-09-971-020-3
; Sequence 3, Application US/09971020
; Patent No. US20020108143A1
; GENERAL INFORMATION:
; APPLICANT: Sano, Hiroshi
; APPLICANT: Kusano, Tomonobu
; APPLICANT: Koizumi, No. US20020108143A1om
; TITLE OF INVENTION: Theobromine Synthase Polypeptide of Coffee Plant and the Gene
; TITLE OF INVENTION: Encoding Said Polypeptide
; FILE REFERENCE: 026350-068
; CURRENT APPLICATION NUMBER: US/09/971,020
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2000-307,149
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Coffea arabica
US-09-971-020-3

Query Match 87.8%; Score 36; DB 3; Length 385;
Best Local Similarity 85.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
|:||||:|
Db 228 CKGDECD 234

RESULT 5
US-09-971-020-5
; Sequence 5, Application US/09971020
; Patent No. US20020108143A1
; GENERAL INFORMATION:
; APPLICANT: Sano, Hiroshi
; APPLICANT: Kusano, Tomonobu
; APPLICANT: Koizumi, No. US20020108143A1om
; TITLE OF INVENTION: Theobromine Synthase Polypeptide of Coffee Plant and the Gene
; TITLE OF INVENTION: Encoding Said Polypeptide
; FILE REFERENCE: 026350-068
; CURRENT APPLICATION NUMBER: US/09/971,020
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2000-307,149
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Coffea arabica
US-09-971-020-5

Query Match 87.8%; Score 36; DB 3; Length 385;
Best Local Similarity 85.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
|:||||:|
Db 228 CKGDECD 234

RESULT 6
US-10-802-773-3
; Sequence 3, Application US/10802773
; Publication No. US20040154055A1
; GENERAL INFORMATION:
; APPLICANT: Sano, Hiroshi
; APPLICANT: Kusano, Tomonobu
; APPLICANT: Koizumi, Nozomu
; TITLE OF INVENTION: Theobromine Synthase Polypeptide of Coffee Plant and the Gene
; TITLE OF INVENTION: Gene Encoding Said Polypeptide
; FILE REFERENCE: 026350-091
; CURRENT APPLICATION NUMBER: US/10/802,773
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: JP 2000-307,149
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Coffea arabica
US-10-802-773-3

Query Match 87.8%; Score 36; DB 4; Length 385;
Best Local Similarity 85.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
|:||||:|
Db 228 CKGDECD 234

RESULT 7
US-10-802-773-5
; Sequence 5, Application US/10802773

```
; Publication No. US20040154055A1
; GENERAL INFORMATION:
; APPLICANT: Sano, Hiroshi
; APPLICANT: Kusano, Tomonobu
; APPLICANT: Koizumi, Nozomu
; TITLE OF INVENTION: Theobromine Synthase Polypeptide of Coffee Plant and the
; TITLE OF INVENTION: Gene Encoding Said Polypeptide
; FILE REFERENCE: 026350-091
; CURRENT APPLICATION NUMBER: US/10/802,773
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: JP 2000-307,149
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Coffea arabica
US-10-802-773-5

Query Match      87.8%; Score 36; DB 4; Length 385;
Best Local Similarity 85.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CKGDEVD 7
Db      228 CKGDEFD 234

RESULT 8
US-10-732-923-10503
; Sequence 10503, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 10503
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Coffea arabica
US-10-732-923-10503

Query Match      87.8%; Score 36; DB 5; Length 385;
Best Local Similarity 85.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CKGDEVD 7
Db      228 CKGDEFD 234

RESULT 9
US-10-732-923-10504
; Sequence 10504, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 10504
; LENGTH: 385
; TYPE: PRT
```

```
; ORGANISM: Coffea arabica
US-10-732-923-10504

Query Match      87.8%; Score 36; DB 5; Length 385;
Best Local Similarity 85.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CKGDEVD 7
Db      228 CKGDECD 234

RESULT 10
US-10-732-923-10505
; Sequence 10505, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 10505
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Coffea arabica
US-10-732-923-10505

Query Match      87.8%; Score 36; DB 5; Length 385;
Best Local Similarity 85.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CKGDEVD 7
Db      228 CKGDECD 234

RESULT 11
US-10-732-923-10506
; Sequence 10506, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 10506
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Coffea arabica
US-10-732-923-10506

Query Match      87.8%; Score 36; DB 5; Length 385;
Best Local Similarity 85.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CKGDEVD 7
Db      228 CKGDEFD 234

RESULT 12
US-10-424-599-257727
; Sequence 257727, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
```

```
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 257727
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_74751C.1.pep
US-10-424-599-257727

Query Match      85.4%; Score 35; DB 4; Length 51;
Best Local Similarity 71.4%; Pred. No. 52;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
Db 13 CKGDDLD 19

RESULT 13
US-10-767-701-57012
; Sequence 57012, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 57012
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 30952297.pep
US-10-767-701-57012

Query Match      85.4%; Score 35; DB 4; Length 103;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CKGDEV 6
Db 37 CKGDEV 42

RESULT 14
US-10-425-115-330473
; Sequence 330473, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
```

```
; SEQ ID NO 330473
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_64492C.1.pep
US-10-425-115-330473

Query Match      85.4%; Score 35; DB 4; Length 393;
Best Local Similarity 71.4%; Pred. No. 3.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
Db 323 CKGDDLD 329

RESULT 15
US-10-424-599-193383
; Sequence 193383, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 193383
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_1664C.1.pep
US-10-424-599-193383

Query Match      85.4%; Score 35; DB 4; Length 521;
Best Local Similarity 85.7%; Pred. No. 4.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
Db 512 CKSDEVD 518

Search completed: December 27, 2005, 11:52:03
Job time : 130.5 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2005, 11:36:08 ; Search time 13.4167 Seconds
(without alignments)
3.721 Million cell updates/sec

Title: US-09-473-619D-2

Perfect score: 41

Sequence: 1 CKGDEVD 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 54001 seqs, 7132810 residues

Total number of hits satisfying chosen parameters: 54001

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB pep.*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep.*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB pep.*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB pep.*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB pep.*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB pep.*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB pep.*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	73.2	9	6	US-10-981-873-20
2	30	73.2	14	6	US-10-981-873-49
3	30	73.2	14	6	US-10-981-873-50
4	30	73.2	18	6	US-10-981-873-10
5	30	73.2	20	6	US-10-981-873-8
6	30	73.2	20	6	US-10-981-873-78
7	29	70.7	65	7	US-11-108-841-11
8	29	70.7	267	6	US-10-495-597-5
9	29	70.7	312	6	US-10-495-597-6
10	29	70.7	395	7	US-11-087-227-4
11	29	70.7	410	7	US-11-087-227-2
12	29	70.7	516	6	US-10-486-968-52
13	29	70.7	1066	7	US-11-055-822-370
14	29	70.7	1066	7	US-11-055-822-1002
15	29	70.7	1113	7	US-11-055-822-368
16	29	70.7	1113	7	US-11-055-822-1000
17	29	70.7	1160	6	US-10-131-826A-234
18	28	68.3	225	6	US-10-467-657-2276
19	28	68.3	360	6	US-10-467-657-5722
20	28	68.3	700	6	US-10-995-561-922
21	28	68.3	700	6	US-10-995-561-924
22	28	68.3	963	6	US-10-995-561-923
23	28	68.3	1011	7	US-11-069-642-111
24	28	68.3	1018	7	US-11-067-121-17
25	28	68.3	1036	6	US-10-131-826A-142

26 65.9 8 7 US-11-069-858-9
27 65.9 17 7 US-11-006-031-29
28 65.9 45 6 US-10-957-887B-40
29 65.9 226 6 US-10-793-626-1932
30 65.9 250 7 US-11-054-515-899
31 65.9 269 6 US-10-131-826A-532
32 65.9 286 6 US-10-793-626-2322
33 65.9 353 6 US-10-641-678-77
34 65.9 411 6 US-10-793-626-3236
35 65.9 486 6 US-10-416-047-14
36 65.9 529 6 US-10-821-234-1520
37 65.9 741 6 US-10-793-626-1178
38 65.9 944 6 US-10-793-626-3324
39 65.9 1115 7 US-11-113-751-46
40 65.9 1133 7 US-11-113-751-48
41 65.9 4128 6 US-10-770-726-77
42 63.4 67 6 US-10-467-657-4358
43 63.4 102 6 US-10-816-768-60
44 63.4 129 6 US-10-793-626-2340
45 63.4 129 7 US-11-116-144-96

ALIGNMENTS

RESULT 1
US-10-981-873-20
; Sequence 20, Application US/10981873
; Publication No. US20050250680A1
; GENERAL INFORMATION:
; APPLICANT: Walensky, Loren D.
; APPLICANT: Korsmeyer, Stanley J.
; APPLICANT: Verdine, Gregory
; TITLE OF INVENTION: STABILIZED ALPHA HELICAL PEPTIDES AND
; TITLE OF INVENTION: USSES THEREOF
; FILE REFERENCE: 00530-124001
; CURRENT APPLICATION NUMBER: US/10/981,873
; CURRENT FILING DATE: 2004-11-05
; PRIOR FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/517,848
; PRIOR FILING DATE: 2004-07-27
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-981-873-20

Query Match 73.2%; Score 30; DB 6; Length 9;
Best Local Similarity 71.4%; Pred. No. 4.1e+04;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
Db 3 CKGDEMD 9

RESULT 2
US-10-981-873-49
; Sequence 49, Application US/10981873
; Publication No. US20050250680A1
; GENERAL INFORMATION:
; APPLICANT: Walensky, Loren D.
; APPLICANT: Korsmeyer, Stanley J.
; APPLICANT: Verdine, Gregory
; TITLE OF INVENTION: STABILIZED ALPHA HELICAL PEPTIDES AND
; TITLE OF INVENTION: USSES THEREOF
; FILE REFERENCE: 00530-124001
; CURRENT APPLICATION NUMBER: US/10/981,873
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: US 60/517,848

; PRIOR FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/591,548
; PRIOR FILING DATE: 2004-07-27
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Naturally occurring peptide
US-10-981-873-49

Query Match 73.2%; Score 30; DB 6; Length 14;
Best Local Similarity 71.4%; Pred. No. 1.6;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
| |||||
Db 6 CIGDEMD 12

RESULT 3
US-10-981-873-50
; Sequence 50, Application US/10981873
; Publication No. US20050250680A1
; GENERAL INFORMATION:
; APPLICANT: Walensky, Loren D.
; APPLICANT: Korsmeyer, Stanley J.
; APPLICANT: Verdine, Gregory
; TITLE OF INVENTION: STABILIZED ALPHA HELICAL PEPTIDES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 00530-124001
; CURRENT APPLICATION NUMBER: US/10/981,873
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: US 60/517,848
; PRIOR FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/591,548
; PRIOR FILING DATE: 2004-07-27
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Naturally occurring peptide
US-10-981-873-50

Query Match 73.2%; Score 30; DB 6; Length 14;
Best Local Similarity 71.4%; Pred. No. 1.6;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
| |||||
Db 6 CIGDEMD 12

RESULT 4
US-10-981-873-10
; Sequence 10, Application US/10981873
; Publication No. US20050250680A1
; GENERAL INFORMATION:
; APPLICANT: Walensky, Loren D.
; APPLICANT: Korsmeyer, Stanley J.
; APPLICANT: Verdine, Gregory
; TITLE OF INVENTION: STABILIZED ALPHA HELICAL PEPTIDES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 00530-124001
; CURRENT APPLICATION NUMBER: US/10/981,873
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: US 60/517,848
; PRIOR FILING DATE: 2003-11-05

; PRIOR APPLICATION NUMBER: US 60/591,548
; PRIOR FILING DATE: 2004-07-27
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Naturally occurring peptide
US-10-981-873-10

Query Match 73.2%; Score 30; DB 6; Length 18;
Best Local Similarity 71.4%; Pred. No. 2;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
| |||||
Db 8 CIGDEMD 14

RESULT 5
US-10-981-873-8
; Sequence 8, Application US/10981873
; Publication No. US20050250680A1
; GENERAL INFORMATION:
; APPLICANT: Walensky, Loren D.
; APPLICANT: Korsmeyer, Stanley J.
; APPLICANT: Verdine, Gregory
; TITLE OF INVENTION: STABILIZED ALPHA HELICAL PEPTIDES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 00530-124001
; CURRENT APPLICATION NUMBER: US/10/981,873
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: US 60/517,848
; PRIOR FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/591,548
; PRIOR FILING DATE: 2004-07-27
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Naturally occurring peptide
US-10-981-873-8

Query Match 73.2%; Score 30; DB 6; Length 20;
Best Local Similarity 71.4%; Pred. No. 2.2;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
| |||||
Db 11 CIGDEMD 17

RESULT 6
US-10-981-873-78
; Sequence 78, Application US/10981873
; Publication No. US20050250680A1
; GENERAL INFORMATION:
; APPLICANT: Walensky, Loren D.
; APPLICANT: Korsmeyer, Stanley J.
; APPLICANT: Verdine, Gregory
; TITLE OF INVENTION: STABILIZED ALPHA HELICAL PEPTIDES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 00530-124001
; CURRENT APPLICATION NUMBER: US/10/981,873
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: US 60/517,848
; PRIOR FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/591,548


```
; PRIOR FILING DATE: 2004-07-27
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Naturally occurring peptide
US-10-981-873-78

Query Match          73.2%; Score 30; DB 6; Length 20;
Best Local Similarity 71.4%; Pred. No. 2.2;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
   |:::|
Db 11 CIGDEMD 17

RESULT 7
US-11-108-841-11
; Sequence 11, Application US/11108841
; Publication No. US20050260657A1
; GENERAL INFORMATION:
; APPLICANT: MIKOSHIBA, Katsuhiko
; APPLICANT: HATTORI, Mitsuhiro
; APPLICANT: HIGO, Takayasu
; TITLE OF INVENTION: A Molecular Entity for Controlling a Calcium
; FILE REFERENCE: 123530
; CURRENT APPLICATION NUMBER: US/11/108,841
; CURRENT FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: JP 2004-124443
; PRIOR FILING DATE: 2004-04-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-11-108-841-11

Query Match          70.7%; Score 29; DB 7; Length 65;
Best Local Similarity 57.1%; Pred. No. 11;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEVD 7
   |:::|
Db 34 CSGDKMD 40

RESULT 8
US-10-495-597-5
; Sequence 5, Application US/10495597
; Publication No. US2005025544A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Vind, Jesper
; APPLICANT: Heldt-Hansen, Hans Peter
; APPLICANT: Erlandsen, Luise
; TITLE OF INVENTION: Lipolytic Enzyme Variants and Method for their Production
; FILE REFERENCE: 10248.204-US
; CURRENT APPLICATION NUMBER: PCT/DK03/00028
; CURRENT FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US/10/495,597
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/353,557
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: DK 2002 00074
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5

Query Match          70.7%; Score 29; DB 6; Length 312;
Best Local Similarity 83.3%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEV 6
   |:::|
Db 279 CTGDEV 284

RESULT 10
US-11-087-227-4
; Sequence 4, Application US/11087227
; Publication No. US20050260566A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Timothy J.
; APPLICANT: Malinowski, Douglas P.
; APPLICANT: Taylor, Adriann J.
; APPLICANT: Parker, Margaret R.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; DETECTION OF CERVICAL DISEASE
; FILE REFERENCE: 046143/287139
; CURRENT APPLICATION NUMBER: US/11/087,227
; CURRENT FILING DATE: 2005-03-23
; PRIOR APPLICATION NUMBER: 60/556,495
; PRIOR FILING DATE: 2004-03-24
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-087-227-4
```

Query Match 70.7%; Score 29; DB 7; Length 395;
 Best Local Similarity 66.7%; Pred. No. 57;
 Matches 4; Conservative 1; Mismatches 0; Gaps 0;

Qy 1 CKGDEV 6
 | |||:
 Db 206 CSGDEI 211

RESULT 11
 US-11-087-227-2
 ; Sequence 2, Application US/11087227
 ; Publication No. US20050260566A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fischer, Timothy J.
 ; APPLICANT: Malinowski, Douglas P.
 ; APPLICANT: Taylor, Adriann J.
 ; APPLICANT: Parker, Margaret R.
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
 ; TITLE OF INVENTION: DETECTION OF CERVICAL DISEASE
 ; FILE REFERENCE: 046143/287139
 ; CURRENT APPLICATION NUMBER: US/11/087,227
 ; CURRENT FILING DATE: 2005-03-23
 ; PRIOR APPLICATION NUMBER: 60/556,495
 ; PRIOR FILING DATE: 2004-03-24
 ; NUMBER OF SEQ ID NOS: 90
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 410
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-087-227-2

Query Match 70.7%; Score 29; DB 7; Length 410;
 Best Local Similarity 66.7%; Pred. No. 59;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEV 6
 | |||:
 Db 221 CSGDEI 226

RESULT 12
 US-10-486-968-52
 ; Sequence 52, Application US/10486968
 ; Publication No. US20050250205A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Genoplate-Valor S.A.S
 ; TITLE OF INVENTION: Use of associations between at least one nucleic sequence
 ; TITLE OF INVENTION: polymorphism of the SH2 gene and at least one seed
 ; TITLE OF INVENTION: quality characteristic in plant selection methods
 ; FILE REFERENCE: SH2
 ; CURRENT APPLICATION NUMBER: US/10/486,968
 ; CURRENT FILING DATE: 2004-02-17
 ; NUMBER OF SEQ ID NOS: 52
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 52
 ; LENGTH: 516
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 US-10-486-968-52

Query Match 70.7%; Score 29; DB 6; Length 516;
 Best Local Similarity 57.1%; Pred. No. 74;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEV 7
 | |||:|
 Db 19 CEGDGID 25

RESULT 13

US-11-055-822-370
 ; Sequence 370, Application US/11055822
 ; Publication No. US20050260707A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pompejus, Markus
 ; APPLICANT: Kroger, Burkhard
 ; APPLICANT: Schroder, Hartwig
 ; APPLICANT: Zelder, Oskar
 ; APPLICANT: Haberhauer, Gregor
 ; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
 ; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
 ; FILE REFERENCE: BGI-121CPCN
 ; CURRENT APPLICATION NUMBER: US/11/055,822
 ; CURRENT FILING DATE: 2005-02-11
 ; PRIOR APPLICATION NUMBER: 09/606,740
 ; PRIOR FILING DATE: 2000-06-23
 ; PRIOR APPLICATION NUMBER: 60/141,031
 ; PRIOR FILING DATE: 1999-06-25
 ; PRIOR APPLICATION NUMBER: 60/142,101
 ; PRIOR FILING DATE: 1999-07-02
 ; PRIOR APPLICATION NUMBER: 60/148,613
 ; PRIOR FILING DATE: 1999-08-12
 ; PRIOR APPLICATION NUMBER: 60/187,970
 ; PRIOR FILING DATE: 2000-03-09
 ; PRIOR APPLICATION NUMBER: DE 19930476.9
 ; PRIOR FILING DATE: 1999-07-01
 ; PRIOR APPLICATION NUMBER: DE 19931415.2
 ; PRIOR FILING DATE: 1999-07-08
 ; PRIOR APPLICATION NUMBER: DE 19931418.7
 ; PRIOR FILING DATE: 1999-07-08
 ; PRIOR APPLICATION NUMBER: DE 19931419.5
 ; PRIOR FILING DATE: 1999-07-08
 ; PRIOR APPLICATION NUMBER: DE 19931420.9
 ; PRIOR FILING DATE: 1999-07-08
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 1158
 ; SEQ ID NO 370
 ; LENGTH: 1066
 ; TYPE: PRT
 ; ORGANISM: Corynebacterium glutamicum
 US-11-055-822-370

Query Match 70.7%; Score 29; DB 7; Length 1066;
 Best Local Similarity 83.3%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEV 6
 | |||:
 Db 737 CDGDEV 742

RESULT 14
 US-11-055-822-1002
 ; Sequence 1002, Application US/11055822
 ; Publication No. US20050260707A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pompejus, Markus
 ; APPLICANT: Kroger, Burkhard
 ; APPLICANT: Schroder, Hartwig
 ; APPLICANT: Zelder, Oskar
 ; APPLICANT: Haberhauer, Gregor
 ; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
 ; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
 ; FILE REFERENCE: BGI-121CPCN
 ; CURRENT APPLICATION NUMBER: US/11/055,822
 ; CURRENT FILING DATE: 2005-02-11
 ; PRIOR APPLICATION NUMBER: 09/606,740
 ; PRIOR FILING DATE: 2000-06-23
 ; PRIOR APPLICATION NUMBER: 60/141,031
 ; PRIOR FILING DATE: 1999-06-25
 ; PRIOR APPLICATION NUMBER: 60/142,101
 ; PRIOR FILING DATE: 1999-07-02
 ; PRIOR APPLICATION NUMBER: 60/148,613

; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 1002
; LENGTH: 1066
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-1002

Query Match 70.7%; Score 29; DB 7; Length 1066;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEV 6
| | | | |
Db 737 CDGDEV 742

RESULT 15
US-11-055-822-368
; Sequence 368, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberbauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 368
; LENGTH: 1113
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-368

Query Match 70.7%; Score 29; DB 7; Length 1113;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGDEV 6
| | | | |
Db 784 CDGDEV 789

Search completed: December 27, 2005, 11:37:31
Job time : 14.4167 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2005, 11:36:08 ; Search time 9.58333 Seconds
(without alignments)
3.721 Million cell updates/sec

Title: US-09-473-619D-1

Perfect score: 27

Sequence: 1 GDEVD 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 54001 seqs, 7132810 residues

Total number of hits satisfying chosen parameters: 54001

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications_AA_New.*
- 1: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pbp.*
 - 2: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pbp.*
 - 3: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pbp.*
 - 4: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pbp.*
 - 5: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pbp.*
 - 6: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pbp.*
 - 7: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pbp.*
 - 8: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pbp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	8	7 US-11-069-858-9	Sequence 9, Appli
2	27	100.0	17	7 US-11-006-031-29	Sequence 29, Appl
3	27	100.0	360	6 US-10-467-657-5722	Sequence 5722, Ap
4	27	100.0	486	6 US-10-416-047-14	Sequence 14, Appl
5	27	100.0	529	6 US-10-821-234-1520	Sequence 1520, Ap
6	27	100.0	4128	6 US-10-770-726-77	Sequence 77, Appl
7	26	96.3	859	7 US-11-000-463-423	Sequence 423, App
8	26	96.3	859	7 US-11-000-463-895	Sequence 895, App
9	26	96.3	1015	6 US-10-467-657-180	Sequence 180, App
10	26	96.3	1015	6 US-10-467-657-3764	Sequence 3764, Ap
11	24	88.9	9	6 US-10-981-873-19	Sequence 19, Appl
12	24	88.9	9	6 US-10-981-873-20	Sequence 20, Appl
13	24	88.9	9	6 US-10-981-873-25	Sequence 25, Appl
14	24	88.9	14	6 US-10-981-873-49	Sequence 49, Appl
15	24	88.9	14	6 US-10-981-873-50	Sequence 50, Appl
16	24	88.9	14	6 US-10-981-873-54	Sequence 54, Appl
17	24	88.9	18	6 US-10-981-873-10	Sequence 10, Appl
18	24	88.9	20	6 US-10-981-873-8	Sequence 8, Appl
19	24	88.9	20	6 US-10-981-873-78	Sequence 78, Appl
20	24	88.9	22	6 US-10-981-873-70	Sequence 70, Appl
21	24	88.9	22	6 US-10-981-873-73	Sequence 73, Appl
22	24	88.9	192	6 US-10-981-873-42	Sequence 42, Appl
23	24	88.9	193	6 US-10-467-657-2464	Sequence 2464, Ap
24	24	88.9	343	6 US-10-467-657-4824	Sequence 4824, Ap
25	24	88.9	343	6 US-10-467-657-7256	Sequence 7256, Ap

26	24	88.9	348	6	US-10-467-657-4840	Sequence 4840, Ap
27	24	88.9	364	7	US-11-108-528-38	Sequence 38, Appl
28	24	88.9	365	7	US-11-108-528-36	Sequence 36, Appl
29	24	88.9	387	7	US-11-074-176-232	Sequence 232, App
30	24	88.9	442	7	US-11-074-176-282	Sequence 282, App
31	24	88.9	881	7	US-11-191-374-12	Sequence 12, Appl
32	24	88.9	881	7	US-11-191-375-12	Sequence 12, Appl
33	23	85.2	8	7	US-11-062-186-1	Sequence 1, Appli
34	23	85.2	93	6	US-10-999-866-20	Sequence 20, Appl
35	23	85.2	93	7	US-11-061-821-20	Sequence 20, Appl
36	23	85.2	95	7	US-11-084-554-216	Sequence 216, App
37	23	85.2	97	7	US-11-084-554-212	Sequence 212, App
38	23	85.2	97	7	US-11-084-554-218	Sequence 218, App
39	23	85.2	99	6	US-10-999-866-17	Sequence 17, Appl
40	23	85.2	99	7	US-11-084-554-200	Sequence 200, App
41	23	85.2	107	6	US-11-061-821-17	Sequence 17, Appl
42	23	85.2	107	6	US-10-467-657-2628	Sequence 2628, Ap
43	23	85.2	109	7	US-11-056-186-3	Sequence 3, Appli
44	23	85.2	109	7	US-11-102-621-4	Sequence 4, Appli
45	23	85.2	111	7	US-11-113-424-182	Sequence 182, App

ALIGNMENTS

RESULT 1

US-11-069-858-9
; Sequence 9, Application US/11069858
; Publication No. US20050249682A1
; GENERAL INFORMATION:
; APPLICANT: Buseman-Williams, Janine
; APPLICANT: Huang, Xueying
; APPLICANT: Wang, Hong
; APPLICANT: Whiting, Gary
; TITLE OF INVENTION: Long Lasting Waterproof Sunscreen Comprising Metal Oxide
; TITLE OF INVENTION: Nanoparticles and Peptide Conditioner
; FILE REFERENCE: CH2985 US CIP
; CURRENT APPLICATION NUMBER: US/11/069,859
; CURRENT FILING DATE: 2005-02-28
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Caspase 3 cleavage site
US-11-069-858-9

Query Match 100.0%; Score 27; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+04;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDEVD 5
Db 4 GDEVD 8

RESULT 2

US-11-006-031-29
; Sequence 29, Application US/11006031
; Publication No. US20050272114A1
; GENERAL INFORMATION:
; APPLICANT: Wood, Keith V.
; APPLICANT: Klaubert, Dieter
; APPLICANT: Los, Georgyi V.
; APPLICANT: Bullett, Robert F.
; APPLICANT: McDougall, Mark
; APPLICANT: Zimprich, Chad
; APPLICANT: Promega Corporation
; TITLE OF INVENTION: Substrates for Covalent Tethering to Proteins
; FILE REFERENCE: 341.035US1
; CURRENT APPLICATION NUMBER: US/11/006,031

; CURRENT FILING DATE: 2004-12-06
; PRIOR APPLICATION NUMBER: US 10/768,976
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: US 60/444,094
; PRIOR FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 60/474,659
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US 60/592,499
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A synthetic peptide
US-11-006-031-29

Query Match 100.0%; Score 27; DB 7; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDEVD 5
|
|
|
|
|
Db 6 GDEVD 10

RESULT 3

US-10-467-657-5722
; Sequence 5722, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5722
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5722

Query Match 100.0%; Score 27; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDEVD 5
|
|
|
|
|
Db 233 GDEVD 237

RESULT 4

US-10-416-047-14
; Sequence 14, Application US/10416047
; Publication No. US20050266512A1
; GENERAL INFORMATION:
; APPLICANT: Buckley
; TITLE OF INVENTION: Detection of Proteases and Screening for Protease Inhibitors
; FILE REFERENCE: 63198-1353
; CURRENT APPLICATION NUMBER: US/10/416,047
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: 60/247,160
; PRIOR FILING DATE: 2000-11-07

; PRIOR APPLICATION NUMBER: PCT/CA01/01561
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 486
; TYPE: PRT
; ORGANISM: Aeromonas hydrophila
US-10-416-047-14

Query Match 100.0%; Score 27; DB 6; Length 486;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDEVD 5
|
|
|
|
|
Db 119 GDEVD 123

RESULT 5

US-10-821-234-1520
; Sequence 1520, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1520
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1520

Query Match 100.0%; Score 27; DB 6; Length 529;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDEVD 5
|
|
|
|
|
Db 321 GDEVD 325

RESULT 6

US-10-770-726-77
; Sequence 77, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 77
; LENGTH: 4128
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-770-726-77

Query Match 100.0%; Score 27; DB 6; Length 4128;

```

Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GDEVD 5
      |||||
Db      2709 GDEVD 2713

RESULT 7
US-11-000-463-423
; Sequence 423, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 423
; LENGTH: 859
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-423

Query Match 96.3%; Score 26; DB 7; Length 859;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GDEVD 5
      |||||
Db      249 GDEID 253

RESULT 8
US-11-000-463-895
; Sequence 895, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping

```

```
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3764
; LENGTH: 1015
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3764
```

```
Query Match          96.3%; Score 26; DB 6; Length 1015;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 GDEVD 5
      |||:|
Db      370 GDEID 374
```

```
RESULT 11
US-10-981-873-19
; Sequence 19, Application US/10981873
; Publication No. US20050250680A1
; GENERAL INFORMATION:
; APPLICANT: Walensky, Loren D.
; APPLICANT: Korsmeyer, Stanley J.
; APPLICANT: Verdine, Gregory
; TITLE OF INVENTION: STABILIZED ALPHA HELICAL PEPTIDES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 00530-124001
; CURRENT APPLICATION NUMBER: US/10/981,873
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: US 60/517,848
; PRIOR FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/591,548
; PRIOR FILING DATE: 2004-07-27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-981-873-19
```

```
Query Match          88.9%; Score 24; DB 6; Length 9;
Best Local Similarity 80.0%; Pred. No. 4.1e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 GDEVD 5
      |||:|
Db      5 GDEMD 9
```

```
RESULT 12
US-10-981-873-20
; Sequence 20, Application US/10981873
; Publication No. US20050250680A1
; GENERAL INFORMATION:
; APPLICANT: Walensky, Loren D.
; APPLICANT: Korsmeyer, Stanley J.
; APPLICANT: Verdine, Gregory
; TITLE OF INVENTION: STABILIZED ALPHA HELICAL PEPTIDES AND
```

```
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 00530-124001
; CURRENT APPLICATION NUMBER: US/10/981,873
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: US 60/517,848
; PRIOR FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/591,548
; PRIOR FILING DATE: 2004-07-27
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-981-873-20
```

```
Query Match          88.9%; Score 24; DB 6; Length 9;
Best Local Similarity 80.0%; Pred. No. 4.1e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 GDEVD 5
      |||:|
Db      5 GDEMD 9
```

```
RESULT 13
US-10-981-873-25
; Sequence 25, Application US/10981873
; Publication No. US20050250680A1
; GENERAL INFORMATION:
; APPLICANT: Walensky, Loren D.
; APPLICANT: Korsmeyer, Stanley J.
; APPLICANT: Verdine, Gregory
; TITLE OF INVENTION: STABILIZED ALPHA HELICAL PEPTIDES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 00530-124001
; CURRENT APPLICATION NUMBER: US/10/981,873
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: US 60/517,848
; PRIOR FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/591,548
; PRIOR FILING DATE: 2004-07-27
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-981-873-25
```

```
Query Match          88.9%; Score 24; DB 6; Length 9;
Best Local Similarity 80.0%; Pred. No. 4.1e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 GDEVD 5
      |||:|
Db      5 GDELD 9
```

```
RESULT 14
US-10-981-873-49
; Sequence 49, Application US/10981873
; Publication No. US20050250680A1
; GENERAL INFORMATION:
; APPLICANT: Walensky, Loren D.
; APPLICANT: Korsmeyer, Stanley J.
; APPLICANT: Verdine, Gregory
; TITLE OF INVENTION: STABILIZED ALPHA HELICAL PEPTIDES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 00530-124001
; CURRENT APPLICATION NUMBER: US/10/981,873
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: US 60/517,848
```


; PRIOR FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/591,548
; PRIOR FILING DATE: 2004-07-27
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Naturally occurring peptide
US-10-981-873-49

Query Match 88.9%; Score 24; DB 6; Length 14;
Best Local Similarity 80.0%; Pred. No. 6.7;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDEVD 5
Db 8 GDEMD 12

RESULT 15
US-10-981-873-50
; Sequence 50, Application US/10981873
; Publication No. US20050250680A1
; GENERAL INFORMATION:
; APPLICANT: Walensky, Loren D.
; APPLICANT: Korsmeyer, Stanley J.
; APPLICANT: Verdine, Gregory
; TITLE OF INVENTION: STABILIZED ALPHA HELICAL PEPTIDES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 00530-124001
; CURRENT APPLICATION NUMBER: US/10/981,873
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: US 60/517,848
; PRIOR FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/591,548
; PRIOR FILING DATE: 2004-07-27
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Naturally occurring peptide
US-10-981-873-50

Query Match 88.9%; Score 24; DB 6; Length 14;
Best Local Similarity 80.0%; Pred. No. 6.7;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDEVD 5
Db 8 GDEMD 12

Search completed: December 27, 2005, 11:37:30
Job time : 9.58333 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2005, 11:37:12 ; Search time 92.5 Seconds
(without alignments)
22.585 Million cell updates/sec

Title: US-09-473-619D-1

Perfect score: 27
Sequence: 1 GDEVD 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	6	4	US-10-168-447-4
2	27	100.0	7	4	US-10-165-258-18
3	27	100.0	7	4	US-10-416-418-2
4	27	100.0	7	5	US-10-466-552A-1
5	27	100.0	8	3	US-09-862-224-2
6	27	100.0	8	3	US-09-747-287-235
7	27	100.0	8	3	US-09-747-287-236
8	27	100.0	8	4	US-10-341-979-4
9	27	100.0	8	5	US-10-935-642-65
10	27	100.0	8	6	US-11-074-473-65
11	27	100.0	8	6	US-11-093-873-8
12	27	100.0	14	4	US-10-341-979-8
13	27	100.0	15	3	US-09-916-940-60
14	27	100.0	15	4	US-10-036-550-60
15	27	100.0	15	5	US-10-934-614-60
16	27	100.0	16	3	US-09-747-287-47
17	27	100.0	16	3	US-09-747-287-52
18	27	100.0	16	3	US-09-747-287-56
19	27	100.0	16	3	US-09-747-287-226
20	27	100.0	16	3	US-09-747-287-241
21	27	100.0	16	3	US-09-874-350A-13
22	27	100.0	16	3	US-09-874-350A-18
23	27	100.0	16	3	US-09-874-350A-22
24	27	100.0	16	3	US-09-874-350A-197
25	27	100.0	16	4	US-10-341-979-7
26	27	100.0	17	3	US-09-747-287-48
27	27	100.0	17	3	US-09-747-287-49

28	27	100.0	17	3	US-09-747-287-54	Sequence 54, Appl
29	27	100.0	17	3	US-09-747-287-55	Sequence 55, Appl
30	27	100.0	17	3	US-09-874-350A-20	Sequence 20, Appl
31	27	100.0	17	3	US-09-874-350A-21	Sequence 21, Appl
32	27	100.0	17	4	US-10-768-976-29	Sequence 29, Appl
33	27	100.0	18	3	US-09-747-287-51	Sequence 51, Appl
34	27	100.0	18	3	US-09-747-287-60	Sequence 60, Appl
35	27	100.0	18	3	US-09-747-287-62	Sequence 62, Appl
36	27	100.0	18	3	US-09-747-287-63	Sequence 63, Appl
37	27	100.0	18	3	US-09-747-287-67	Sequence 67, Appl
38	27	100.0	18	3	US-09-747-287-227	Sequence 227, App
39	27	100.0	18	3	US-09-747-287-228	Sequence 228, App
40	27	100.0	18	3	US-09-747-287-232	Sequence 232, App
41	27	100.0	18	3	US-09-747-287-233	Sequence 233, App
42	27	100.0	18	3	US-09-747-287-242	Sequence 242, App
43	27	100.0	18	3	US-09-874-350A-14	Sequence 14, Appl
44	27	100.0	18	3	US-09-874-350A-15	Sequence 15, Appl
45	27	100.0	18	3	US-09-874-350A-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1

US-10-168-447-4
; Sequence 4, Application US/10168447
; Publication No. US20030203404A1
; GENERAL INFORMATION:
; APPLICANT: JOLY, ERIK
; TITLE OF INVENTION: A BIOLUMINESCENCE RESONANCE ENERGY TRANSFER (BRET)
; TITLE OF INVENTION: SYSTEM WITH BROAD SPECTRAL RESOLUTION BETWEEN DONOR AND
; FILE REFERENCE: 13157.125US
; CURRENT APPLICATION NUMBER: US/10/168,447
; PRIOR FILING DATE: 2003-08-25
; PRIOR APPLICATION NUMBER: PCT/CA00/01516
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: CA 2,291,968
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: CA 2,314,861
; PRIOR FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: peptide
US-10-168-447-4

Query Match 100.0%; Score 27; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
| | | | |
Db 1 GDEVD 5

RESULT 2

US-10-165-258-18
; Sequence 18, Application US/10165258
; Publication No. US20030092029A1
; GENERAL INFORMATION:
; APPLICANT: Josephson, Lee
; APPLICANT: Weisleder, Ralph
; APPLICANT: Perez, J. Manuel
; TITLE OF INVENTION: MAGNETIC - NANOPARTICLE CONJUGATES AND METHODS OF USE
; FILE REFERENCE: 00786-537001
; CURRENT APPLICATION NUMBER: US/10/165,258
; CURRENT FILING DATE: 2002-10-15

; PRIOR APPLICATION NUMBER: US 60/296,378
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-416-418-2

Query Match 100.0%; Score 27; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
Db 1 GDEVD 5

RESULT 3

US-10-416-418-2
; Sequence 2, Application US/10416418
; Publication No. US20040115838A1
; GENERAL INFORMATION:
; APPLICANT: Quake, Stephen R.
; APPLICANT: Unger, Marc Alexander
; APPLICANT: Chou, Hou-Pu
; APPLICANT: Thorsen, Todd A.
; APPLICANT: Scherer, Axel
; APPLICANT: California Institute of Technology
; TITLE OF INVENTION: Apparatus and Methods for Conducting Assays and High
; TITLE OF INVENTION: Throughput Screening
; FILE REFERENCE: 20174C-003220PC
; CURRENT APPLICATION NUMBER: US/10/416,418
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/249,327
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: US 60/281,946
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/281,948
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequence
; OTHER INFORMATION: contained in peptide substrate with caspase
; OTHER INFORMATION: cleavage site
US-10-416-418-2

Query Match 100.0%; Score 27; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
Db 1 GDEVD 5

RESULT 4

US-10-466-552A-1
; Sequence 1, Application US/10466552A
; Publication No. US20040241782A1
; GENERAL INFORMATION:
; APPLICANT: Evotec OAI AG
; TITLE OF INVENTION: Methods and Means for the Detection of Enzyme-Catalyzed
; TITLE OF INVENTION: Cleavage and Linking Reactions
; FILE REFERENCE: P69029US0

; CURRENT APPLICATION NUMBER: US/10/466,552A
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: PCT/EP02/00845
; PRIOR FILING DATE: 2002-01-28
; PRIOR APPLICATION NUMBER: EP01101869.4
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized
US-10-466-552A-1

Query Match 100.0%; Score 27; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
Db 1 GDEVD 5

RESULT 5

US-09-862-224-2
; Sequence 2, Application US/09862224
; Publication No. US20030186214A1
; GENERAL INFORMATION:
; APPLICANT: Yan, Xiongwei
; APPLICANT: Miraglia, Sheri
; APPLICANT: Yuan, Pau
; TITLE OF INVENTION: PEPTIDE CONJUGATES AND FLUORESCENCE DETECTION METHODS FOR INTRACEL
; TITLE OF INVENTION: CASPASE ASSAY
; FILE REFERENCE: 4568US
; CURRENT APPLICATION NUMBER: US/09/862,224
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-862-224-2

Query Match 100.0%; Score 27; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
Db 1 GDEVD 5

RESULT 6

US-09-747-287-235
; Sequence 235, Application US/09747287
; Publication No. US20030207264A1
; GENERAL INFORMATION:
; APPLICANT: KOMORIYA, AKIRA
; APPLICANT: PACKARD, BEVERLY S.
; TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
; TITLE OF INVENTION: ACTIVITY IN BIOLOGICAL SAMPLES
; FILE REFERENCE: 300-948600US
; CURRENT APPLICATION NUMBER: US/09/747,287
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/349,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US08/802,981
; PRIOR FILING DATE: 1997-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11

; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 235
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic (chemically synthesized) peptide. Artificial protease
; OTHER INFORMATION: substrate.
US-09-747-287-235

Query Match 100.0%; Score 27; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
|||
Db 1 GDEVD 5

RESULT 7

US-09-747-287-236
; Sequence 236, Application US/09747287
; Publication No. US20030207264A1
; GENERAL INFORMATION:
; APPLICANT: KOMORIYA, AKIRA
; TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
; FILE REFERENCE: ACTIVITY IN BIOLOGICAL SAMPLES
; CURRENT APPLICATION NUMBER: US/09/747,287
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/349,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US08/802,981
; PRIOR FILING DATE: 1997-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 236
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic (chemically synthesized) peptide. Artificial protease
; OTHER INFORMATION: substrate.
US-09-747-287-236

Query Match 100.0%; Score 27; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
|||
Db 1 GDEVD 5

RESULT 8

US-10-341-979-4
; Sequence 4, Application US/10341979
; Publication No. US20040002128A1
; GENERAL INFORMATION:
; APPLICANT: Hong Kong University of Science & Technology
; APPLICANT: Chang, Donald Choy
; APPLICANT: Luo, Qian Kathy
; TITLE OF INVENTION: GFP-BASED METHODS FOR DETECTING APOPTOSIS
; FILE REFERENCE: 32144183-1
; CURRENT APPLICATION NUMBER: US/10/341,979
; CURRENT FILING DATE: 2003-01-11
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4

; LENGTH: 8
; TYPE: PRT
; ORGANISM: mammalian
US-10-341-979-4

Query Match 100.0%; Score 27; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
|||
Db 2 GDEVD 6

RESULT 9

US-10-935-642-65
; Sequence 65, Application US/10935642
; Publication No. US20050050656A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Xueying
; APPLICANT: Wu, Ying
; TITLE OF INVENTION: Peptide-Based Conditioners and Colorants for Hair, Skin, and
; FILE REFERENCE: CL2296 US NA
; CURRENT APPLICATION NUMBER: US/10/935,642
; CURRENT FILING DATE: 2004-09-07
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 65
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Caspase 3 cleavage site
US-10-935-642-65

Query Match 100.0%; Score 27; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
|||
Db 4 GDEVD 8

RESULT 10

US-11-074-473-65
; Sequence 65, Application US/11074473
; Publication No. US20050226839A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Xueying
; APPLICANT: Wang, Hong
; APPLICANT: Wu, Ying
; TITLE OF INVENTION: Peptide-Based Conditioners and Colorants for Hair, Skin, and
; FILE REFERENCE: CL2296 US NA
; CURRENT APPLICATION NUMBER: US/11/074,473
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US/10/935,642
; PRIOR FILING DATE: 2004-09-07
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 65
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Caspase 3 cleavage site
US-11-074-473-65

Query Match 100.0%; Score 27; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
|||||

Db 4 GDEVD 8

RESULT 11
US-11-093-873-8
; Sequence 8, Application US/11093873
; Publication No. US2005029335A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Xueying
; APPLICANT: Kobos, Robert K.
; APPLICANT: Xu, Gann
; TITLE OF INVENTION: Peptide-Based Carbon Nanotube Hair Colorants and Their Use in
; FILE OF INVENTION: Hair Coloring and Cosmetic Compositions
; FILE REFERENCE: CL2610
; CURRENT APPLICATION NUMBER: US/11/093,873
; CURRENT FILING DATE: 2005-03-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Caspase 3 cleavage site
US-11-093-873-8

Query Match 100.0%; Score 27; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
|||||

Db 4 GDEVD 8

RESULT 12
US-10-341-979-8
; Sequence 8, Application US/10341979
; Publication No. US2004002128A1
; GENERAL INFORMATION:
; APPLICANT: Hong Kong University of Science & Technology
; APPLICANT: Chang, Donald Choy
; APPLICANT: Luo, Qian Kathy
; TITLE OF INVENTION: GFP-BASED METHODS FOR DETECTING APOPTOSIS
; FILE REFERENCE: 32144183-1
; CURRENT APPLICATION NUMBER: US/10/341,979
; CURRENT FILING DATE: 2003-01-11
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 14
; TYPE: PRT
; ORGANISM: mammalian
US-10-341-979-8

Query Match 100.0%; Score 27; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
|||||

Db 5 GDEVD 9

RESULT 13
US-09-916-940-60
; Sequence 60, Application US/09916940
; Patent No. US20020127564A1
; GENERAL INFORMATION:

; APPLICANT: No. US20020127564A1Alan, Garry P
; TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR
; FILE REFERENCE: A-64260-6/RMS/AMS
; CURRENT APPLICATION NUMBER: US/09/916,940
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 09/727,715
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 08/963,368
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: US 08/589,109
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: US 08/589,911
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: US 08/789,333
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: US 08/787,738
; PRIOR FILING DATE: 1997-01-23
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: anti-apoptosis
; OTHER INFORMATION: sequence.
US-09-916-940-60

Query Match 100.0%; Score 27; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
|||||

Db 6 GDEVD 10

RESULT 14
US-10-096-550-60
; Sequence 60, Application US/10096550
; Publication No. US20030170641A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030170641Alan, Garry P
; APPLICANT: Rothenburg, Michael S.
; TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT EFFECTOR
; FILE REFERENCE: A-64259-1 correction
; CURRENT APPLICATION NUMBER: US/10/096,550
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 08/787,738
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 08/589,108
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: 08/589,911
; PRIOR FILING DATE: 1996-01-23
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic.
US-10-096-550-60

Query Match 100.0%; Score 27; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
|||||

Db 6 GDEVD 10

```

RESULT 15
US-10-934-614-60
; Sequence 60, Application US/10934614
; Publication No. US20050037415A1
; GENERAL INFORMATION:
; APPLICANT: Nolan, Garry P
; APPLICANT: Rothenburg, Michael S.
; TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT EFFECTOR
; TITLE OF INVENTION: PEPTIDES AND RNA MOLECULES
; FILE REFERENCE: A-64259-1 correction
; CURRENT APPLICATION NUMBER: US/10/934,614
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: US/10/096,550
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 08/787,738
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 08/589,108
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: 08/589,911
; PRIOR FILING DATE: 1996-01-23
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 60
; TYPE: PRT
; LENGTH: 15
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic.
US-10-934-614-60

```

```

Query Match      100.0%; Score 27; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 GDEVD 5
Db      6 GDEVD 10

```

```

Search completed: December 27, 2005, 11:52:02
Job time : 93.5 secs

```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2005, 11:36:08 ; Search time 121.667 Seconds
(without alignments)
28.994 Million cell updates/sec

Title: US-09-473-619D-1
Perfect score: 27
Sequence: 1 GDEVD 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	27	100.0	44	2	Q51913_PSEMV	Q51913 pseudomonas
2	27	100.0	49	2	Q96P95_HUMAN	Q96P95 homo sapien
3	27	100.0	57	2	Q8LH38_ORYSA	Q8LH38 oryza sativ
4	27	100.0	62	2	Q981K2_RHILO	Q981K2 rhizobium l
5	27	100.0	65	2	Q8FRE2_COREF	Q8FRE2 corynebacte
6	27	100.0	70	2	Q7TDK9_VIRU	Q7TDK9 halovirus h
7	27	100.0	70	2	Q8V6S0_VIRU	Q8V6S0 halovirus h
8	27	100.0	78	2	Q5KR13_CORGL	Q5KR13 corynebacte
9	27	100.0	84	2	Q8PX54_METWA	Q8PX54 methanosarc
10	27	100.0	84	2	Q5WTM4_LEGPL	Q5WTM4 legionella
11	27	100.0	84	2	Q5X1W3_LEGPA	Q5X1W3 legionella
12	27	100.0	84	2	Q5ZSE1_LEGPH	Q5ZSE1 legionella
13	27	100.0	87	2	Q9R605_ECOLI	Q9R605 escherichia
14	27	100.0	94	2	Q7PQ03_ANOGA	Q7PQ03 anopheles g
15	27	100.0	95	2	Q3VTW6_DROME	Q3VTW6 drosophila
16	27	100.0	97	2	P82379_STOCA	P82379 stomoxys ca
17	27	100.0	101	2	Q6Y8V6_ORYSA	Q6Y8V6 oryza sativ
18	27	100.0	103	2	Q656T4_ORYSA	Q656T4 oryza sativ
19	27	100.0	103	2	Q93EX2_NOOCA	Q93EX2 rhodococcus
20	27	100.0	104	2	Q4X8C0_PLACH	Q4X8C0 plasmodium
21	27	100.0	105	2	Q94GH9_ORYSA	Q94GH9 oryza sativ
22	27	100.0	110	2	Q6ZL08_ORYSA	Q6ZL08 oryza sativ
23	27	100.0	121	2	Q51PX3_WAGGR	Q51PX3 magnaporthe
24	27	100.0	128	1	RS6E_HALMA	P21509 haloarcula
25	27	100.0	128	2	Q5RZ79_BACT	Q5RZ79 uncultured
26	27	100.0	129	2	Q54W83_DICDI	Q54W83 dictyosteli
27	27	100.0	131	2	Q9A1S3_STRPY	Q9A1S3 streptococc
28	27	100.0	132	2	Q6Q7D9_ORYSA	Q6Q7D9 oryza sativ
29	27	100.0	133	2	Q6GBY0_STAAS	Q6GBY0 staphylococ
30	27	100.0	133	2	Q6GJG3_STAAR	Q6GJG3 staphylococ
31	27	100.0	133	2	Q5HIG7_STAAC	Q5HIG7 staphylococ

32	27	100.0	133	2	Q7A1S0_STAAM	Q7A1S0 staphylococ
33	27	100.0	133	2	Q7A7A7_STAAM	Q7A7A7 staphylococ
34	27	100.0	133	2	Q99W95_STAAM	Q99W95 staphylococ
35	27	100.0	137	2	Q4Q860_LEIMA	Q4Q860 leishmania
36	27	100.0	142	2	Q4KL07_MOUSE	Q4KL07 mus musculu
37	27	100.0	147	2	Q72BJ0_DESVH	Q72BJ0 desulfovibr
38	27	100.0	148	1	KAD6_THEAC	Q9hkm7 thermoplas
39	27	100.0	151	1	D1D4_YEAST	P36108 saccharomyc
40	27	100.0	154	1	Y194_AQUAE	Q66575 aquifex aeo
41	27	100.0	154	2	Q978Y3_THEVO	Q978Y3 thermoplas
42	27	100.0	154	2	Q8SB19_ORYSA	Q8SB19 oryza sativ
43	27	100.0	155	1	RS15_HALMA	P05762 haloarcula
44	27	100.0	158	2	O85494_HELFE	O85494 helicobacte
45	27	100.0	158	2	P87658_ADEN	P87658 duck adenov

ALIGNMENTS

RESULT 1
Q51913_PSEMV
ID Q51913_PSEMV PRELIMINARY; PRT; 44 AA.
AC Q51913;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE HMG-CoA-reductase (Fragment).
OS Pseudomonas mevalonii.
OC Bacteria; Proteobacteria.
OX NCBI_TaxID=32044;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=30078086; PubMed=2687236;
RA Anderson D.H., Rodwell V.W.;
RT "Nucleotide sequence and expression in Escherichia coli of the 3-hydroxy-3-methylglutaryl coenzyme A lyase gene of Pseudomonas mevalonii.";
RL J. Bacteriol. 171:6468-6472(1989).
DR EMBL; M31807; AAA25894.1; -; Genomic_DNA.
DR HSPP; P13702; 10AX.
DR GO; GO:0004420; F:hydroxymethylglutaryl-CoA reductase (NADPH) . . .; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
DR InterPro; IPR002202; HMG-CoA_red.
DR Pfam; PF00368; HMG-CoA_red; 1.
FT NON TER 1 1
SQ SEQUENCE 44 AA; 4925 MW; 9722E2A58DEE9193 CRC64;

Query Match 100.0%; Score 27; DB 2; Length 44;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDEVD 5
Db 13 GDEVD 17

RESULT 2
Q96P95_HUMAN
ID Q96P95_HUMAN PRELIMINARY; PRT; 49 AA.
AC Q96P95;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Poly(ADP-ribose) polymerase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kang H.S., Park Y.J., Jung H.M., Jun D.Y., Huh T.L., Kim Y.H.;

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF012118; AAL02174.1; -: mRNA.
 DR GO: GO:0005634; C:nucleus; IEA.
 DR GO: GO:0003677; F:DNA binding; IEA.
 DR InterPro: IPR001510; Znf_PolyADPpol.
 DR Pfam: PF00645; zf-PARP; 1.
 DR ProDom: PD004675; Znf_PolyADPpol; 1.
 DR PROSITE: PS50064; PARP_ZN_FINGER_2; 1.
 FT NON_TER 1 49
 FT NON_TER 49 49
 SQ SEQUENCE 49 AA; 5300 MW; 68F91B7ADABDF4A5 CRC64;

Query Match 100.0%; Score 27; DB 2; Length 49;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDEVD 5
 Db 33 GDEVD 37

RESULT 3

Q8LH38 ORYSA PRELIMINARY; PRT; 57 AA.
 AC Q8LH38;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Hypothetical protein P0617C02.128 (Hypothetical protein B1317D11.123).
 DE B1317D11.123).
 GN Name=P0617C02.128; Synonym=B1317D11.123;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriocarpaceae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Saeki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, PAC clone:P0617C02.";
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Saeki T., Matsumoto T., Katayose Y.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, BAC clone:B1317D11.";
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AP004673; BAC10385.1; -: Genomic DNA.
 DR EMBL: AP006186; BAC31949.1; -: Genomic DNA.
 DR Gramene; Q8LH38; -;
 KW Hypothetical protein.
 SQ SEQUENCE 57 AA; 6286 MW; 581BE65ECAB6E787 CRC64;

Query Match 100.0%; Score 27; DB 2; Length 57;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDEVD 5
 Db 26 GDEVD 30

RESULT 4

Q981K2 RHIL0 PRELIMINARY; PRT; 62 AA.
 AC Q981K2;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Msl9339 protein.
 GN OrderedLocusNames=msl9339;
 OS Rhizobium loti (Mesorhizobium loti).

OG Plasmid pMLa.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Phyllobacteriaceae; Mesorhizobium.
 OX NCBI_TaxID=381;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=MAFF303099;
 RC MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti.";
 RT Mesorhizobium loti.";
 RL DNA Res. 7:331-338 (2000).
 DR EMBL: BA000013; BAB54707.1; -: Genomic DNA.
 DR InterPro: IPR008162; Pyrophosphatase.
 DR PROSITE: PS00387; PPASE; UNKNOWN_1.
 KW Complete proteome; Plasmid.
 SQ SEQUENCE 62 AA; 6855 MW; CC089E57239F833D CRC64;

Query Match 100.0%; Score 27; DB 2; Length 62;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDEVD 5
 Db 43 GDEVD 47

RESULT 5

Q8FRE2 COREF PRELIMINARY; PRT; 65 AA.
 AC Q8FRE2;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=CE0819;
 OS Corynebacterium efficiens.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
 OX NCBI_TaxID=152794;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Y8-314 / AJ 12310 / DSM 44549 / JCM 11189;
 RC MEDLINE=22723752; PubMed=12840036; DOI=10.1101/gr.1285603;
 RA Nishio Y., Nakamura Y., Kawarabayashi Y., Usuda Y., Kimura E.,
 RA Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
 RA Gojobori T.;
 RT "Comparative complete genome sequence analysis of the amino acid replacements responsible for the thermostability of Corynebacterium efficiens.";
 RT efficiens.";
 RL Genome Res. 13:1572-1579 (2003).
 DR EMBL: BA000035; BAC17629.1; -: Genomic DNA.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 65 AA; 7245 MW; 5FCE714480188C72 CRC64;

Query Match 100.0%; Score 27; DB 2; Length 65;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDEVD 5
 Db 19 GDEVD 23

RESULT 6

Q7TDK9_9VIRU PRELIMINARY; PRT; 70 AA.
 ID Q7TDK9_9VIRU
 AC Q7TDK9;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)

```

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Halovirus HF1.
OC Viruses; unclassified viruses; Haloviruses.
OX NCBI_TaxID=222645;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15090523; DOI=10.1128/JB.186.9.2810-2817.2004;
RA Tang S.-L., Nuttall S., Dyal-Smith M.;
RT "Haloviruses HF1 and HF2: Evidence for a Recent and Large
Recombination Event."; 2817(2004).
RL J. Bacteriol. 186:2810-2817(2004).
DR EMBL; AY190604; AA061332.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 70 AA; 7583 MW; 64BCED165C9C761A CRC64;

Query Match 100.0%; Score 27; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDEVD 5
Db 21 GDEVD 25

RESULT 7
Q8V6S0_9VIRU
ID Q8V6S0_9VIRU PRELIMINARY; PRT; 70 AA.
AC Q8V6S0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Halovirus HF2.
OC Viruses; unclassified viruses; Haloviruses.
OX NCBI_TaxID=33771;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21964609; PubMed=11967086;
RA Tang S.-L., Nuttall S., Ngui K., Fisher C., Lopez P., Dyal-Smith M.;
RT "HF2: A double-stranded DNA tailed haloarchaeal virus with a mosaic
genome.";
RL Mol. Microbiol. 44:283-296(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Tang S.-L., Fisher C., Ngui K., Nuttall S.D., Dyal-Smith M.L.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF222060; AAL54955.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 70 AA; 7583 MW; 64BCED165C9C761A CRC64;

Query Match 100.0%; Score 27; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDEVD 5
Db 21 GDEVD 25

RESULT 8
Q5KRI3_CORGL
ID Q5KRI3_CORGL PRELIMINARY; PRT; 78 AA.
AC Q5KRI3;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;

```

```

RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=R;
RA Suzuki N., Okayama S., Nonaka H., Tauge Y., Inui M., Yukawa H.;
RT "Large-Scale Engineering of the Corynebacterium glutamicum Genome.";
RL Appl. Environ. Microbiol. 71:3369-3372(2005).
DR EMBL; AB193035; BAD84070.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 78 AA; 8315 MW; D9EC323EB05D638E CRC64;

Query Match 100.0%; Score 27; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDEVD 5
Db 35 GDEVD 39

RESULT 9
Q8PX54_METWA
ID Q8PX54_METWA PRELIMINARY; PRT; 84 AA.
AC Q8PX54;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Glutaredoxin-like protein.
GN OrderedLocusNames=MM1368;
OS Methanosarcina mazei (Methanosarcina frisia).
OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2209;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Goel / G01 / ATCC BAA-199 / DSM 3647 / OCM 88;
RX MEDLINE=22120827; PubMed=12125824;
RA Deppenmeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,
RA Martinez-Arias R., Henne A., Wieser A., Baeumer S., Jacobi C.,
RA Brueggemann H., Lienard T., Christmann A., Boemecke M., Steckel S.,
RA Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
RA Fritz H.-J., Gottschalk G.;
RT "The genome of Methanosarcina mazei: evidence for lateral gene
transfer between Bacteria and Archaea.";
RL J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
DR EMBL; AE013370; AAM31064.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 84 AA; 9434 MW; 4C3FD1FF9AE4C796 CRC64;

Query Match 100.0%; Score 27; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDEVD 5
Db 72 GDEVD 76

RESULT 10
Q5WTM4_LEGPL
ID Q5WTM4_LEGPL PRELIMINARY; PRT; 84 AA.
AC Q5WTM4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=ipl2500;
OS Legionella pneumophila (strain Lens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=297245;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15467720; DOI=10.1038/ng1447;

```

```

RA Cazalet C., Rusniok C., Brueggemann H., Zidane N., Magnier A., Ma L.,
RA Tichit M., Jarraud S., Bouchier C., Vandenesch F., Kunst F.,
RA Etienne J., Glaeser P., Buchrieser C.;
RT "Evidence in the Legionella pneumophila genome for exploitation of
RT host cell functions and high genome plasticity.";
RL Nat. Genet. 36:1165-1173(2004).
DR EMBL; CRG28337; CAH16740.1; -; Genomic_DNA.
DR Legiolist; lpl2500; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 84 AA; 9418 MW; BBFF63D0BF6B5731 CRC64;

Query Match 100.0%; Score 27; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDEVD 5
Db 39 GDEVD 43

RESULT 11
Q5X1W3_LEGPA
ID Q5X1W3_LEGPA PRELIMINARY; PRT; 84 AA.
AC Q5X1W3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=lp2630;
OS Legionella pneumophila (strain Paris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=297246;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15467720; DOI=10.1038/ngl1447;
RA Cazalet C., Rusniok C., Brueggemann H., Zidane N., Magnier A., Ma L.,
RA Tichit M., Jarraud S., Bouchier C., Vandenesch F., Kunst F.,
RA Etienne J., Glaeser P., Buchrieser C.;
RT "Evidence in the Legionella pneumophila genome for exploitation of
RT host cell functions and high genome plasticity.";
RL Nat. Genet. 36:1165-1173(2004).
DR EMBL; CRG28336; CAH13783.1; -; Genomic_DNA.
DR Legiolist; lp2630; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 84 AA; 9418 MW; BBFF63D0BF6B5731 CRC64;

Query Match 100.0%; Score 27; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDEVD 5
Db 39 GDEVD 43

RESULT 12
Q5ZSEI_LEGPH
ID Q5ZSEI_LEGPH PRELIMINARY; PRT; 84 AA.
AC Q5ZSEI;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=lp2578;
OS Legionella pneumophila subsp. pneumophila (strain Philadelphia 1 /
OS ATCC 33152).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=272624;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15448271; DOI=10.1126/science.1099776;

```

```

RA Chien M., Morozova I., Shi S., Sheng H., Chen J., Gomez S.M.,
RA Asamani G., Hill K., Nuara J., Feder M., Rineer J., Greenberg J.J.,
RA Steshenko V., Park S.H., Zhao B., Tepitskaya E., Edwards J.R.,
RA Pampou S., Georgiou A., Chou I.-C., Iannuccilli W., Ulz M.E.,
RA Kim D.H., Geringer-Sameth A., Goldsberry C., Morozov P., Fischer S.G.,
RA Segal G., Qu X., Rzhetsky A., Zhang P., Cavanis E., De Jong P.J.,
RA Ju J., Kalachikov S., Shuman H.A., Russo J.J.;
RT "The genomic sequence of the accidental pathogen Legionella
RT pneumophila.";
RL Science 305:1966-1968(2004).
DR EMBL; AE017354; AAU28636.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 84 AA; 9418 MW; BBFF63D0BF6B5731 CRC64;

Query Match 100.0%; Score 27; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDEVD 5
Db 39 GDEVD 43

RESULT 13
Q9R605_ECOLI
ID Q9R605_ECOLI PRELIMINARY; PRT; 87 AA.
AC Q9R605;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Adaptive response regulator PHOP (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX Medline=93146391; PubMed=1490612; DOI=10.1016/0378-1097(92)90042-M;
RA Wren B.W., Colby S.M., Cumberley R.R., Pallen M.J.;
RT "Generate PCR primers for the amplification of fragments from genes
RT encoding response regulators from a range of pathogenic bacteria.";
RL FEMS Microbiol. Lett. 78:287-291(1992).
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:000156; F:two-component response regulator activity; IEA.
DR GO; GO:0007600; P:sensory perception; IEA.
DR GO; GO:0000160; P:two-component signal transduction system (p. . .); IEA.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF00072; Response_reg; 1.
DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS0110; RESPONSE_REGULATORY; 1.
KW Sensory transduction.
SQ SEQUENCE 87 AA; 9734 MW; 4F7B55F552FA5EDF CRC64;

Query Match 100.0%; Score 27; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDEVD 5
Db 16 GDEVD 20

RESULT 14
Q7PQ03_ANOGA
ID Q7PQ03_ANOGA PRELIMINARY; PRT; 94 AA.
AC Q7PQ03;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP0000010025 (Fragment).
GN ORFNames=ENSANGG0000007536;
OS Anopheles gambiae str. PEST.

```

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culicidae;
 OC Anophelinae; Anopheles.
 OX NCBI_TaxID=180454;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PEST;
 RG "Anopheles gambiae Sequence Committee;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 RN Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PEST;
 RG "Anopheles gambiae Sequence Committee;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAB01008900; EAA09471.2; -; Genomic_DNA.
 DR HSSP; P62314; 1834.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0005732; C:small nucleolar ribonucleoprotein complex; IEA.
 DR GO; GO:0006397; P:mRNA processing; IEA.
 DR InterPro; IPR006649; snRNP.
 DR Pfam; PF01423; LSM; 1.
 DR ProDom; PD020287; snRNP; 1.
 FT NON TER 1
 SQ SEQUENCE 94 AA; 10606 MW; 006D6B57067E2873 CRC64;
 Query/Match 100.0%; Score 27; DB 2; Length 94;
 Best Local Similarity 100.0%; Pred. No. 5.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy ~ 1 GDEVD 5
 Db 73 GDEVD 77
 RESULT 15
 Q9VW6 DROME
 ID Q9VW6 DROME PRELIMINARY; PRT; 95 AA.
 AC Q9VW6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE CG10418-PA (GM14851p).
 GN ORFNames=CG10418, CG10418;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champagne B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Balwle R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brattler P.,
 RA Burtis K.C., Bueam D.A., Butler H., Cadenhead E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleeb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC MEDLINE=22436065; PubMed=12537568;
 RA Celnik S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
 RA Pacleeb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
 RT melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC MEDLINE=22436070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celnik S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 RT a genomics perspective.";
 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC MEDLINE=22436069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradscky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celnik S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC Berkeley Drosophila Genome Project;
 RA Celnik S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
 RA Hoskins R., Stapleton M., Pacleeb J., Park S., Svirskas R., Smith E.,
 RA Yu C., Rubin G.;
 RT "Drosophila melanogaster release 4 sequence.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC FlyBase;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacleeb J., Paragas V., Park S.,

RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -!- INTERACTION:
CC Q9W087:CG2021; NbExp=1; IntAct=EBI-150361, EBI-140047;
CC Q9W2K2:CG4279; NbExp=1; IntAct=EBI-150361, EBI-85740;
CC O18353:Chi; NbExp=1; IntAct=EBI-150361, EBI-130074;
DR EMBL; AE003541; AAF4929.1; -; Genomic_DNA.
DR EMBL; AY070862; AAL48484.1; -; mRNA.
DR HSSP; P62314; 1B34.
DR IntAct; Q9VTW6; -.
DR Ensemble; CG10418; Drosophila melanogaster.
DR FlyBase; FBgn0036277; CG10418.
DR GO; GO:0005688; C:snRNP U6; NAS.
DR InterPro; IPR006649; snRNP.
DR InterPro; IPR001163; snRNP_Sm.
DR Pfam; PF01423; LSM; 1.
DR ProDom; PD020287; snRNP; 1.
DR SMART; SM00651; Sm; 1.
SQ SEQUENCE 95 AA; 10737 MW; 0B9AA86FEE54CBCF CRC64;

Query Match 100.0%; Score 27; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDEVD 5
Db 74 GDEVD 78

Search completed: December 27, 2005, 11:48:16
Job time : 124.667 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2005, 11:36:08 ; Search time 27.0833 Seconds
(without alignments)
15.263 Million cell updates/sec

Title: US-09-473-619D-1
Perfect score: 27
Sequence: 1 GDEVD 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5-COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6-COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H-COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCTUS-COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE-COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	8	2	US-08-802-981-178
2	27	100.0	8	2	US-08-802-981-188
3	27	100.0	8	2	US-09-747-287A-235
4	27	100.0	8	2	US-09-747-287A-236
5	27	100.0	8	2	US-09-394-019C-189
6	27	100.0	12	2	US-08-665-643A-3
7	27	100.0	12	2	US-09-522-666-11
8	27	100.0	15	2	US-08-789-333F-60
9	27	100.0	15	2	US-08-787-738B-60
10	27	100.0	15	2	US-09-916-940-60
11	27	100.0	15	2	US-10-096-550-60
12	27	100.0	16	2	US-08-802-981-48
13	27	100.0	16	2	US-08-802-981-172
14	27	100.0	16	2	US-09-747-287A-47
15	27	100.0	16	2	US-09-747-287A-52
16	27	100.0	16	2	US-09-747-287A-56
17	27	100.0	16	2	US-09-747-287A-226
18	27	100.0	16	2	US-09-747-287A-241
19	27	100.0	16	2	US-09-394-019C-12
20	27	100.0	16	2	US-09-394-019C-17
21	27	100.0	16	2	US-09-394-019C-21
22	27	100.0	16	2	US-09-394-019C-180
23	27	100.0	16	2	US-09-394-019C-225
24	27	100.0	16	2	US-09-394-019C-229
25	27	100.0	16	2	US-09-394-019C-262
26	27	100.0	16	2	US-09-394-019C-266
27	27	100.0	17	2	US-09-522-666-27

28	27	100.0	17	2	US-09-747-287A-48	Sequence 48, Appl
29	27	100.0	17	2	US-09-747-287A-49	Sequence 49, Appl
30	27	100.0	17	2	US-09-747-287A-54	Sequence 54, Appl
31	27	100.0	17	2	US-09-747-287A-55	Sequence 55, Appl
32	27	100.0	17	2	US-09-394-019C-19	Sequence 19, Appl
33	27	100.0	17	2	US-09-394-019C-20	Sequence 20, Appl
34	27	100.0	17	2	US-09-394-019C-227	Sequence 227, App
35	27	100.0	17	2	US-09-394-019C-228	Sequence 228, App
36	27	100.0	17	2	US-09-394-019C-264	Sequence 264, App
37	27	100.0	17	2	US-09-394-019C-265	Sequence 265, App
38	27	100.0	18	2	US-08-802-981-49	Sequence 49, Appl
39	27	100.0	18	2	US-08-802-981-50	Sequence 50, Appl
40	27	100.0	18	2	US-08-802-981-54	Sequence 54, Appl
41	27	100.0	18	2	US-08-802-981-173	Sequence 173, App
42	27	100.0	18	2	US-08-802-981-174	Sequence 174, App
43	27	100.0	18	2	US-09-747-287A-51	Sequence 51, Appl
44	27	100.0	18	2	US-09-747-287A-60	Sequence 60, Appl
45	27	100.0	18	2	US-09-747-287A-62	Sequence 62, Appl

ALIGNMENTS

RESULT 1

US-08-802-981-178
; Sequence 178, Application US/08802981
; Patent No. 6037137
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of Enzyme
; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 231
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/802,981
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 016865-0003000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 178:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-802-981-178

Query Match 100.0%; Score 27; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDEVD 5

Db 1 GDEVD 5

```
RESULT 2
US-08-802-981-188
; Sequence 188, Application US/08802981
; Patent No. 6037137
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; TITLE OF INVENTION: Compositions for the Detection of Enzyme
; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 231
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/802,981
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 016865-0003000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 188:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-802-981-188

Query Match 100.0%; Score 27; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
Db 1 GDEVD 5

RESULT 3
US-09-747-287A-235
; Sequence 235, Application US/09747287A
; Patent No. 6893868
; GENERAL INFORMATION:
; APPLICANT: KOMORIYA, AKIRA
; TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
; TITLE OF INVENTION: ACTIVITY IN BIOLOGICAL SAMPLES
; FILE REFERENCE: 300-948600US
; CURRENT APPLICATION NUMBER: US/09/747,287A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/349,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US08/802,981
; PRIOR FILING DATE: 1997-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 235

Query Match 100.0%; Score 27; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
Db 1 GDEVD 5

RESULT 4
US-09-747-287A-236
; Sequence 236, Application US/09747287A
; Patent No. 6893868
; GENERAL INFORMATION:
; APPLICANT: KOMORIYA, AKIRA
; TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
; TITLE OF INVENTION: ACTIVITY IN BIOLOGICAL SAMPLES
; FILE REFERENCE: 300-948600US
; CURRENT APPLICATION NUMBER: US/09/747,287A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/349,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US08/802,981
; PRIOR FILING DATE: 1997-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 236
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic (chemically synthesized) peptide. Artificial protease
; OTHER INFORMATION: substrate.
US-09-747-287A-236

Query Match 100.0%; Score 27; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
Db 1 GDEVD 5

RESULT 5
US-09-394-019C-189
; Sequence 189, Application US/09394019C
; Patent No. 6936687
; GENERAL INFORMATION:
; APPLICANT: Oncoimmunin, Inc.
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
; TITLE OF INVENTION: SAMPLES AND METHODS OF USE THEREOF
; FILE REFERENCE: 300-903820US
; CURRENT APPLICATION NUMBER: US/09/394,019C
; CURRENT FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: PCT/US98/00300
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: US 08/802,981
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 405
```

```
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic (chemically synthesized) peptide. Artificial protease
; OTHER INFORMATION: substrate.
US-09-747-287A-235

Query Match 100.0%; Score 27; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
Db 1 GDEVD 5

RESULT 4
US-09-747-287A-236
; Sequence 236, Application US/09747287A
; Patent No. 6893868
; GENERAL INFORMATION:
; APPLICANT: KOMORIYA, AKIRA
; TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
; TITLE OF INVENTION: ACTIVITY IN BIOLOGICAL SAMPLES
; FILE REFERENCE: 300-948600US
; CURRENT APPLICATION NUMBER: US/09/747,287A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/349,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US08/802,981
; PRIOR FILING DATE: 1997-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 236
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic (chemically synthesized) peptide. Artificial protease
; OTHER INFORMATION: substrate.
US-09-747-287A-236

Query Match 100.0%; Score 27; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
Db 1 GDEVD 5

RESULT 5
US-09-394-019C-189
; Sequence 189, Application US/09394019C
; Patent No. 6936687
; GENERAL INFORMATION:
; APPLICANT: Oncoimmunin, Inc.
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
; TITLE OF INVENTION: SAMPLES AND METHODS OF USE THEREOF
; FILE REFERENCE: 300-903820US
; CURRENT APPLICATION NUMBER: US/09/394,019C
; CURRENT FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: PCT/US98/00300
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: US 08/802,981
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 405
```



```
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 189
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide substrate
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Artificial/Unknown = central protease recognition domain
US-09-394-019C-189

Query Match      100.0%; Score 27; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GDEVD 5
Db      1 GDEVD 5
        |||||

RESULT 6
US-08-665-643A-3
; Sequence 3, Application US/08665643A
; Patent No. 6288037
; GENERAL INFORMATION:
; APPLICANT: Talanian, Robert V.
; APPLICANT: Hodges, John C.
; TITLE OF INVENTION: SUBSTRATES AND INHIBITORS FOR CYSTEINE PROTEASE ICH-1
; FILE REFERENCE: BBI-049CPCPA
; CURRENT APPLICATION NUMBER: US/08/665,643A
; PRIOR FILING DATE: 1996-06-18
; PRIOR APPLICATION NUMBER: 08/592,943
; PRIOR FILING DATE: 1996-01-29
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; OTHER INFORMATION: amino-terminal acetyl modification;
; OTHER INFORMATION: carboxy-terminal amide modification
US-08-665-643A-3

Query Match      100.0%; Score 27; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GDEVD 5
Db      2 GDEVD 6
        |||||

RESULT 7
US-09-522-666-11
; Sequence 11, Application US/09522666
; Patent No. 633167
; GENERAL INFORMATION:
; APPLICANT: Shuey, David
; APPLICANT: Quinet, Elaine
; TITLE OF INVENTION: Methods and Reagents for Identifying Inhibitors of
; FILE REFERENCE: 6-00
; CURRENT APPLICATION NUMBER: US/09/522,666
; CURRENT FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 12
```

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequence
; OTHER INFORMATION: encoding g-g linkers and caspase-3 cleavage
; OTHER INFORMATION: sites
US-09-522-666-11

Query Match      100.0%; Score 27; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GDEVD 5
Db      7 GDEVD 11
        |||||

RESULT 8
US-08-789-333F-60
; Sequence 60, Application US/08789333F
; Patent No. 6153380
; GENERAL INFORMATION:
; APPLICANT: No. 6153380an, Garry P
; APPLICANT: Rothenberg, S. M.
; TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR
; TITLE OF INVENTION: EFFECTOR PEPTIDES AND RNA MOLECULES
; FILE REFERENCE: A642601DJBRMSDSS
; CURRENT APPLICATION NUMBER: US/08/789,333F
; CURRENT FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: 08/589,108
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: 08/589,911
; PRIOR FILING DATE: 1996-01-23
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: anti-apoptosis
; OTHER INFORMATION: sequence.
US-08-789-333F-60

Query Match      100.0%; Score 27; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GDEVD 5
Db      6 GDEVD 10
        |||||

RESULT 9
US-08-787-738B-60
; Sequence 60, Application US/08787738B
; Patent No. 6455247
; GENERAL INFORMATION:
; APPLICANT: No. 6455247an, Garry P
; APPLICANT: Rothenberg, Michael S.
; TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT EFFECTOR
; TITLE OF INVENTION: PEPTIDES AND RNA MOLECULES
; FILE REFERENCE: A-64259-1 correction
; CURRENT APPLICATION NUMBER: US/08/787,738B
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 08/589,108
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: 08/589,911
; PRIOR FILING DATE: 1996-01-23
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 15
```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic.
US-08-787-738B-60

Query Match 100.0%; Score 27; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
|
|
|
|
Db 6 GDEVD 10

RESULT 10
US-09-916-940-60
; Sequence 60, Application US/09916940
; Patent No. 6737241
; GENERAL INFORMATION:
; APPLICANT: No. 6737241an, Garry P
; TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR
; FILE REFERENCE: A-64260-6/RMS/RMS
; CURRENT APPLICATION NUMBER: US/09/916,940
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 08/727,715
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 08/963,368
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: US 08/589,109
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: US 08/589,911
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: US 08/789,333
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: US 08/787,738
; PRIOR FILING DATE: 1997-01-23
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 15

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: anti-apoptosis
; OTHER INFORMATION: sequence.
US-09-916-940-60

Query Match 100.0%; Score 27; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
|
|
|
|
Db 6 GDEVD 10

RESULT 11
US-10-096-550-60
; Sequence 60, Application US/10096550
; Patent No. 6833245
; GENERAL INFORMATION:
; APPLICANT: No. 6833245an, Garry P
; APPLICANT: Rothenburg, Michael S.
; TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT EFFECTOR
; FILE REFERENCE: A-64259-1 correction
; CURRENT APPLICATION NUMBER: US/10/096,550
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 08/787,738
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 08/589,108

; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: 08/589,911
; PRIOR FILING DATE: 1996-01-23
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic.
US-10-096-550-60

Query Match 100.0%; Score 27; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
|
|
|
|
Db 6 GDEVD 10

RESULT 12
US-08-802-981-48
; Sequence 48, Application US/08802981
; Patent No. 6037137
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of Enzyme
; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 231
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/802,981
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 016865-000300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "xaa = 9-fluorenylmethoxycarbonyl (Fmoc) group attached
; OTHER INFORMATION: to the alpha-amino group of Lys"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /product= "Aib"
US-08-802-981-48

Query Match 100.0%; Score 27; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
Db 4 GDEVD 8

RESULT 13
US-08-981-172
; Sequence 172, Application US/08802981
; Patent No. 6037137
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; TITLE OF INVENTION: Compositions for the Detection of Enzyme
; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 231
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/802,981
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 016865-0003000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 172:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = 9-fluorenylmethoxycarbonyl (Fmoc) group attached
; OTHER INFORMATION: to the alpha-amino and 5'-carboxytetramethylrhodamine attached
; OTHER INFORMATION: the epsilon-amino group of Lys"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /product= "Alb"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 14
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = 5'-carboxytetramethylrhodamine attached to the
; OTHER INFORMATION: epsilon-amino group of Lys"
; US-08-981-172

Query Match 100.0%; Score 27; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
Db 4 GDEVD 8

RESULT 14
US-09-747-287A-47
; Sequence 47, Application US/09747287A
; Patent No. 6893868
; GENERAL INFORMATION:
; APPLICANT: KOMORIYA, AKIRA
; TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
; TITLE OF INVENTION: ACTIVITY IN BIOLOGICAL SAMPLES
; FILE REFERENCE: 300-948600US
; CURRENT APPLICATION NUMBER: US/09/747,287A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/349,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US08/802,981
; PRIOR FILING DATE: 1997-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 47
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide.
; US-09-747-287A-47

Query Match 100.0%; Score 27; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
Db 4 GDEVD 8

RESULT 15
US-09-747-287A-52
; Sequence 52, Application US/09747287A
; Patent No. 6893868
; GENERAL INFORMATION:
; APPLICANT: KOMORIYA, AKIRA
; TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
; TITLE OF INVENTION: ACTIVITY IN BIOLOGICAL SAMPLES
; FILE REFERENCE: 300-948600US
; CURRENT APPLICATION NUMBER: US/09/747,287A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/349,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US08/802,981
; PRIOR FILING DATE: 1997-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 52
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide.
; NAME/KEY: misc feature
; LOCATION: (4)_(4)
; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid
; FEATURE:

```
; NAME/KEY: misc_feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (16)..(16)
; OTHER INFORMATION: K is blocked with amide
US-09-747-287A-52
```

```
Query Match      100.0%; Score 27; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. NO. 21;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GDEVD 5
        |||||
Db       5 GDEVD 9
```

Search completed: December 27, 2005, 11:38:42
Job time : 28.0833 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2005, 11:36:08 ; Search time 19.1667 Seconds
(without alignments)
25.100 Million cell updates/sec

Title: US-09-473-619D-1

Perfect score: 27

Sequence: 1 GDEVD 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	16	2	PL0137
2	27	100.0	44	2	B43714
3	27	100.0	133	2	E89817
4	27	100.0	134	2	A55580
5	27	100.0	135	1	R3HS13
6	27	100.0	151	2	S37812
7	27	100.0	154	2	C70318
8	27	100.0	156	1	R3HS11
9	27	100.0	199	2	S17777
10	27	100.0	228	2	T04945
11	27	100.0	233	1	F69078
12	27	100.0	237	2	T46121
13	27	100.0	257	2	T25387
14	27	100.0	267	2	A69319
15	27	100.0	268	2	H83051
16	27	100.0	343	2	B66468
17	27	100.0	349	2	AB1715
18	27	100.0	349	2	AG1344
19	27	100.0	352	2	E70249
20	27	100.0	355	2	C95843
21	27	100.0	359	2	T16350
22	27	100.0	371	2	H97073
23	27	100.0	376	2	S76145
24	27	100.0	382	2	AG1161
25	27	100.0	385	2	JC2256
26	27	100.0	385	2	G72659
27	27	100.0	387	2	H69080
28	27	100.0	393	2	T05532
29	27	100.0	411	2	F90215

30	27	100.0	413	2	T07110
31	27	100.0	413	2	JE0142
32	27	100.0	420	2	H84182
33	27	100.0	423	2	E84027
34	27	100.0	425	2	T41172
35	27	100.0	428	2	A44756
36	27	100.0	436	2	G69466
37	27	100.0	440	2	A96564
38	27	100.0	453	2	A96688
39	27	100.0	455	2	H69230
40	27	100.0	463	2	T39621
41	27	100.0	485	2	S26575
42	27	100.0	486	2	A25976
43	27	100.0	486	2	T47647
44	27	100.0	488	2	S26576
45	27	100.0	489	2	T39672

ALIGNMENTS

RESULT 1

PL0137
protein kinase, 80K - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 18-Jun-1993
C;Accession: PL0137
R;Dechert, U.; Weber, M.; Weber-Schaeuffelen, M.; Wollny, E.
J. Neurochem. 53, 1268-1275, 1989
A;Title: Isolation and partial characterization of an 80,000-dalton protein kinase from t

A;Reference number: PL0137; MUID:89361455; PMID:2769266

A;Accession: PL0137

A;Molecule type: protein

A;Residues: 1-16 <DEC>

A;Cross-references: UNIPARC:UPI0000177D3E

C;Comment: This protein has a novel serine/threonine-specific protein kinase activity.

Query Match 100.0%; Score 27; DB 2; Length 16;

Best Local Similarity 100.0%; Pred. No. 10;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDEVD 5

Db 1 GDEVD 5

RESULT 2

B43714
hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) - Pseudomonas sp. (fragment)

C;Species: Pseudomonas sp.

C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 26-May-2000

C;Accession: B43714

R;Anderson, D.H.; Rodwell, V.W.

J. Bacteriol. 171, 6468-6472, 1989

A;Title: Nucleotide sequence and expression in Escherichia coli of the 3-hydroxy-3-methyl

A;Reference number: A43714; MUID:90078086; PMID:2687236

A;Accession: B43714

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-44 <AND>

A;Cross-references: UNIPARC:UPI00000BD792; GB:M31807; NID:g151370; PIDN:AAA25894.1; PID:5

C;Superfamily: Methanococcus jannaschii hydroxymethylglutaryl-CoA reductase (NADPH)

C;Keywords: coenzyme A; oxidoreductase

Query Match 100.0%; Score 27; DB 2; Length 44;

Best Local Similarity 100.0%; Pred. No. 29;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDEVD 5

Db 13 GDEVD 17

RESULT 3

E89817
hypothetical protein SA0466 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: E89817
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A>Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311152; PMID:11418146
A:Accession: E89817
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-133 <KUR>
A:Cross-references: UNIPROT:Q99W95; UNIPARC:UPI0000054639; GB:BA000018; PID:gl3700398; E
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA0466
C:Superfamily: polyribonucleotide nucleotidyltransferase homolog yabR

Query Match 100.0%; Score 27; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
|
|
|
|
DB 53 GDEVD 57

RESULT 4

A55580
dihydrodipicolinate reductase (EC 1.3.1.26) - Pseudomonas aeruginosa (fragment)
C:Species: Pseudomonas aeruginosa
C>Date: 25-Aug-1995 #sequence_revision 25-Aug-1995 #text_change 09-Jul-2004
C:Accession: A55580
R:Kwon, D.H.; Lu, C.D.; Walthall, D.A.; Brown, T.M.; Houghton, J.E.; Abdelal, A.T.
J. Bacteriol. 176, 2532-2542, 1994
A>Title: Structure and regulation of the carAB operon in Pseudomonas aeruginosa and Pseu
A:Reference number: A55580; MUID:94222830; PMID:8169201
A:Accession: A55580
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-134 <KNO>
A:Cross-references: UNIPROT:P38103; UNIPARC:UPI000016FC7F; GB:U04992; NID:G451649; PIDN
A:Note: authors translated the codon CAG for residue 128 as Glu
C:Genetics:
A:Gene: dapB
C:Superfamily: dihydrodipicolinate reductase
C:Keywords: diaminopimelate-lysine biosynthesis; NAD; oxidoreductase
F;22-26/Region: substrate binding

Query Match 100.0%; Score 27; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
|
|
|
|
DB 11 GDEVD 15

RESULT 5

R3HS13
ribosomal protein S6.eR [validated] - Haloarcula marismortui
N:Alternate names: ribosomal protein HS13
C:Species: Haloarcula marismortui
C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C:Accession: S11593
R:Kimura, M.; Arndt, E.; Hatakeyama, T.; Hatakeyama, T.; Kimura, J.
Can. J. Microbiol. 35, 195-199, 1989
A>Title: Ribosomal proteins in halobacteria.
A:Reference number: S11593; MUID:89248680; PMID:2655851

A:Accession: S11593
A:Molecule type: protein
A:Residues: 1-135 <KIM>
A:Cross-references: UNIPROT:P21509; UNIPARC:UPI00000135089
A:Note: the source is designated as Halobacterium marismortui
C:Superfamily: Haloarcula ribosomal protein HS13
C:Keywords: protein biosynthesis; ribosome

Query Match 100.0%; Score 27; DB 1; Length 135;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
|
|
|
|
DB 47 GDEVD 51

RESULT 6

S37812
hypothetical protein YKL002w - Yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C:Accession: S37812; S37813
R:Duesterhoeft, A.; Moestl, D.; Poehlmann, R.; Philippsen, P.
submitted to the Protein Sequence Database, March 1994
A:Reference number: S37811
A:Accession: S37812
A:Molecule type: DNA
A:Residues: 1-151 <DUE>
A:Cross-references: UNIPROT:P36108; UNIPARC:UPI000013B6A4; EMBL:Z28002; NID:G485988; PIDP
A:Experimental source: strain S288C
R:Boyer, J.; Pascolo, S.; Richard, G.F.; Ghazvini, M.; Colleaux, L.; Thierry, A.; Monnier
submitted to the Protein Sequence Database, March 1994
A:Reference number: S37813
A:Accession: S37813
A:Molecule type: DNA
A:Residues: 1-151 <BOY>
A:Cross-references: UNIPARC:UPI000013B6A4; EMBL:Z28002; NID:G485988; PIDN:CAA81834.1; PII
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:DID4
A:Cross-references: SGD:S0001485
A:Map position: 11L

Query Match 100.0%; Score 27; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 11e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
|
|
|
|
DB 74 GDEVD 78

RESULT 7

C70318
hypothetical protein aq_194 - Aquifex aeolicus
C:Species: Aquifex aeolicus
C>Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C:Accession: C70318
R:Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ove
V.
Nature 392, 353-358, 1998
A>Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: C70318
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-154 <AQF>
A:Cross-references: UNIPROT:O66575; UNIPARC:UPI00000562BA; GB:AE000677; NID:G2982900; PII
A:Experimental source: strain VF5
C:Genetics:
A:Gene: aq_194
C:Superfamily: Aquifex aeolicus hypothetical protein aq_194

Query Match 100.0%; Score 27; DB 2; Length 154;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
 |||||
 Db 64 GDEVD 68

RESULT 8
 R3HS11
 ribosomal protein S15 [validated] - Haloarcula marismortui
 N;Alternate names: ribosomal protein HS11; ribosomal protein HS13.er
 C;Species: Haloarcula marismortui
 C;Date: 31-Dec-1998 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
 C;Accession: A31906; A23602
 R;Arndt, E.; Kimura, M.
 J. Biol. Chem. 263, 16063-16068, 1988
 A;Title: Molecular cloning and nucleotide sequence of the gene for the ribosomal protein
 A;Reference number: A92677; MUID:89034064; PMID:3182783
 A;Accession: A31906
 A;Molecule type: DNA
 A;Residues: 1-156 <ARN>
 A;Cross-references: UNIPROT:P05762; UNIPARC:UPI000016P7CF; GB:J04062; NID:G148809; PIDN:
 R;Arndt, E.; Breithaupt, G.; Kimura, M.
 FEBS Lett. 194, 227-234, 1986
 A;Title: The complete amino acid sequence of ribosomal protein H-S11 from the archaeobact
 A;Reference number: A23602
 A;Accession: A23602
 A;Molecule type: protein
 A;Residues: 2-25, 'A', 27-156 <ARN2>
 A;Cross-references: UNIPARC:UPI0000173A3B
 A;Note: the source is given as Halobacterium marismortui
 C;Superfamily: rat ribosomal protein S13; eubacterial ribosomal protein S15 homology
 C;Keywords: protein biosynthesis; ribosome
 F;2-156/Product: ribosomal protein S13.er #status experimental <MAT>
 F;86-151/Domain: eubacterial ribosomal protein S15 homology <ES15>

Query Match 100.0%; Score 27; DB 1; Length 156;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
 |||||
 Db 135 GDEVD 139

RESULT 9
 S1777
 strG protein - Streptomyces griseus
 C;Species: Streptomyces griseus
 C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
 C;Accession: S17777
 R;Mansouri, K.; Piepersberg, W.
 Mol. Gen. Genet. 228, 459-469, 1991
 A;Title: Genetics of streptomycin production in Streptomyces griseus: nucleotide sequenc
 A;Reference number: S17775; MUID:91375432; PMID:1654502
 A;Accession: S17777
 A;Status: not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 1-199 <MAN>
 A;Cross-references: UNIPROT:P09398; UNIPARC:UPI000013613F; GB:Y00459; NID:g16
 C;Genetics:
 A;Gene: strG

Query Match 100.0%; Score 27; DB 2; Length 199;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
 |||||
 Db 73 GDEVD 77

RESULT 10

T04945
 hypothetical protein F7J7.80 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C;Accession: T04945
 R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.
 submitted to the Protein Sequence Database, July 1998
 A;Reference number: Z15391
 A;Accession: T04945

A;Molecule type: DNA
 A;Residues: 1-228 <BEV>

A;Cross-references: UNIPROT:O49555; UNIPARC:UPI000000A5AAS; EMBL:AL021960
 A;Experimental source: cultivar Columbia; BAC clone F7J7
 C;Genetics:

A;Map position: 4
 A;Note: F7J7.80

C;Superfamily: Arabidopsis thaliana hypothetical protein F7J7.80

Query Match 100.0%; Score 27; DB 2; Length 228;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
 |||||
 Db 59 GDEVD 63

RESULT 11

F69078
 Probable formate acetyltransferase activating enzyme (SC 1.97.1.4) - Methanobacterium the
 N;Alternate names: formate C-acetyltransferase activating enzyme; pyruvate formate-lyase
 C;Species: Methanobacterium thermoautotrophicum
 C;Date: 15-Jan-1999 #sequence_revision 15-Jan-1999 #text_change 09-Jul-2004
 C;Accession: F69078

R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; F
 ; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.;
 ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 J. Bacteriol. 179, 7135-7155, 1997

A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functi
 A;Reference number: A69000; MUID:98037514; PMID:9371463

A;Accession: F69078
 A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-233 <MTH>

A;Cross-references: UNIPROT:O27623; UNIPARC:UPI00000665A2; GB:AE000918; NID:

A;Experimental source: strain Delta H

C;Genetics:

A;Gene: MTH1586

A;Start codon: GTG

C;Superfamily: Methanococcus probable pyruvate formate-lyase activating enzyme

C;Keywords: iron; metalloprotein; oxidoreductase

F;29,33,36/Binding site: iron (Cy8) #status predicted

Query Match 100.0%; Score 27; DB 1; Length 233;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
 |||||
 Db 45 GDEVD 49

RESULT 12

T46121

hypothetical protein T2J13.70 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004

C;Accession: T46121

R;Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Mayer, K.
 submitted to the Protein Sequence Database, November 1999

A;Reference number: Z23023
 A;Accession: T46121
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-237 <RIE>
 A;Cross-references: UNIPROT:Q9SMU6; UNIPARC:UPI000000AA900; EMBL:AL132967
 A;Experimental source: cultivar Columbia; BAC clone T2J13
 C;Genetics:
 A;Map position: 3
 A;Note: T2J13.70

Query Match 100.0%; Score 27; DB 2; Length 237;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
 DB 153 GDEVD 157

RESULT 13

T25387
 hypothetical protein T27F6.7 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Dec-2004
 C;Accession: T25387
 R;Dobson, R.
 submitted to the EMBL Data Library, November 1996
 A;Reference number: Z20026
 A;Accession: T25387
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-257 <WIL>
 A;Cross-references: UNIPROT:O45871; UNIPARC:UPI0000081671; EMBL:Z82060; PIDN:CAB04886.1;
 A;Experimental source: clone T27F6
 C;Genetics:
 A;Gene: CESP:T27F6.7
 A;Map position: 1
 A;Introns: 98/1; 148/2; 213/3

Query Match 100.0%; Score 27; DB 2; Length 257;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
 DB 26 GDEVD 30

RESULT 14

A69319
 thiamin biosynthesis protein (thiF) homolog - Archaeoglobus fulgidus
 C;Species: Archaeoglobus fulgidus
 C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 16-Aug-2004
 C;Accession: A69319
 R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
 ; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
 Nature 390, 364-370, 1997
 A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiaich, P.; Kaine, B.P.; Sykes, S.
 Smith, H.O.; Woese, C.R.; Venter, J.C.
 A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
 A;Reference number: A69250; MUID:98049343; PMID:9389475
 A;Accession: A69319
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-267 <KLE>
 A;Cross-references: UNIPROT:O29698; UNIPARC:UPI000005707A; GB:AE001066; GB:AE000782; NID
 C;Superfamily: Molybdopter in biosynthesis protein moeb

Query Match 100.0%; Score 27; DB 2; Length 267;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
 DB 61 GDEVD 65

RESULT 15

H83051
 dihydrodipicolinate reductase PA4759 [imported] - Pseudomonas aeruginosa (strain PA01)
 C;Species: Pseudomonas aeruginosa
 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
 C;Accession: H83051
 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.; Brj
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Polger, K.R.; Kas, A.; Larbig, K.; Lim
 ; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
 A;Reference number: A82950; MUID:20437337; PMID:10984043
 A;Accession: H83051
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-268 <STO>
 A;Cross-references: UNIPROT:P38103; UNIPARC:UPI0000128E8C; GB:AE004889; GB:AE004091; NID:
 A;Experimental source: strain PA01
 C;Genetics:
 A;Gene: dapB; PA4759
 C;Superfamily: dihydrodipicolinate reductase

Query Match 100.0%; Score 27; DB 2; Length 268;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
 DB 145 GDEVD 149

Search completed: December 27, 2005, 11:37:03
 Job time : 21.1667 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2005, 11:36:08 ; Search time 111.25 Seconds
(without alignments)
19.747 Million cell updates/sec

Title: US-09-473-619D-1

Perfect score: 27

Sequence: 1 GDEVD 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003s:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	5	2 AAW51892	AAW51892 Peptide u
2	27	100.0	5	2 ABP57518	ABP57518 Different
3	27	100.0	5	6 ABU63411	ABU63411 Caspase-3
4	27	100.0	6	3 AAY54043	AAY54043 Peptide s
5	27	100.0	6	6 ABP57512	ABP57512 Different
6	27	100.0	7	2 AAW51893	AAW51893 Peptide u
7	27	100.0	7	5 AAO18998	AAO18998 Caspase-3
8	27	100.0	8	2 AAW82031	AAW82031 Fluorogen
9	27	100.0	8	2 AAW82030	AAW82030 Fluorogen
10	27	100.0	8	4 AAG73266	AAG73266 Protease
11	27	100.0	8	5 ABU60376	ABU60376 Protease
12	27	100.0	8	5 ABU60473	ABU60473 Central p
13	27	100.0	8	5 ABU60370	ABU60370 Protease
14	27	100.0	8	6 ABP99790	ABP99790 Peptide s
15	27	100.0	8	7 ADM65819	ADM65819 Apoptosis
16	27	100.0	8	9 ADY55660	ADY55660 Caspase 3
17	27	100.0	9	8 ADO05347	ADO05347 Caspase-3
18	27	100.0	9	9 AEA39602	AEA39602 Caspase-3
19	27	100.0	12	2 AAW29954	AAW29954 Cysteine
20	27	100.0	12	2 AAW51894	AAW51894 Sequence
21	27	100.0	12	5 AAU75878	AAU75878 Caspase-3
22	27	100.0	12	6 ABP60485	ABP60485 Caspase 3
23	27	100.0	13	6 ABP99777	ABP99777 Amino aci
24	27	100.0	14	2 AAR34533	AAR34533 Beta-hexo

25	27	100.0	14	3 AAY77498	AAY77498 Caspase a
26	27	100.0	14	4 AAB51228	AAB51228 Fusion pr
27	27	100.0	14	7 ADM65825	ADM65825 Apoptosis
28	27	100.0	15	2 AAW29118	AAW29118 Fas-media
29	27	100.0	15	4 AAB45972	AAB45972 Transdomi
30	27	100.0	15	6 ABG98492	ABG98492 Synthetic
31	27	100.0	15	6 ABU14056	ABU14056 Transdomi
32	27	100.0	15	7 AAE39862	AAE39862 Peptide u
33	27	100.0	15	7 ADD28944	ADD28944 Library i
34	27	100.0	15	8 ADR49006	ADR49006 Caspase r
35	27	100.0	15	8 ADR49004	ADR49004 Caspase r
36	27	100.0	15	9 ADY21077	ADY21077 Transdomi
37	27	100.0	15	9 AEA39607	AEA39607 Conjugate
38	27	100.0	16	2 AAW82237	AAW82237 Fluorogen
39	27	100.0	16	4 AAG73305	AAG73305 Protease
40	27	100.0	16	4 AAG73257	AAG73257 Protease
41	27	100.0	16	4 AAG73301	AAG73301 Protease
42	27	100.0	16	4 AAG73078	AAG73078 Protease
43	27	100.0	16	4 AAG73268	AAG73268 Protease
44	27	100.0	16	4 AAG73087	AAG73087 Protease
45	27	100.0	16	4 AAG73083	AAG73083 Protease

ALIGNMENTS

RESULT 1
AAW51892
ID AAW51892 standard; peptide; 5 AA.

XX AC AAW51892;

XX XX 21-SEP-1998 (first entry)

XX DE Peptide useful for diagnosing diseases that involve apoptosis.

XX KW Immunogen; apoptosis; screen; inhibitor; stimulator; antibody; PARP;
XX KW poly-ADP-ribose polymerase; antibody.

XX OS Mammalia.

XX PN WO9821590-A1.

XX PD 22-MAY-1998.

XX PF 13-NOV-1997; 97WO-US020214.

XX PR 15-NOV-1996; 96US-0030961P.

XX PR 12-NOV-1997; 97US-00967625.

XX (CEPH-) CEPHALON INC.

XX Siman R, Bozyczko-coyne D, Meyer SL, Bhat RV;

XX WPI; 1998-298113/26.

XX Peptide(s) containing epitope(s) characteristic of peptide(s) formed during apoptosis - useful for diagnosing diseases that involve apoptosis and to screen for inhibitors or stimulators of apoptosis.

XX Claim 1; Page 14; 40pp; English.

XX The invention relates to peptides that contain the sequences AAW51892-3. Also claimed are: (1) antibodies that bind specifically to an epitope on a peptide produced by apoptotic cells; (2) a method for identifying inhibitors or stimulators of apoptosis by measuring the effect of a test compound on amount of antibody bound to cell or tissue, and (3) kits for detecting peptides produced by apoptotic cells. Antibodies are used in immunoassays to detect and quantify apoptosis, particularly for diagnosis of apoptosis-associated conditions, e.g. chronic neurodegeneration, cancer, sepsis, trauma to head or spine, hypoxia, anoxia, ischaemia, lesions and exposure to toxins, or susceptibility to such a condition

SQ Sequence 5 AA;

Query Match 100.0%; Score 27; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDEVD 5
 |||||
 Db 1 GDEVD 5

RESULT 2

ABP57518
 ID ABP57518 standard; peptide; 5 AA.

XX

AC ABP57518;

XX 28-APR-2003 (first entry)

XX Differentially isotopically labelled (DiMas) peptide #11.

XX Mass spectrometry; polymer; analysis; cleavage; substrate specificity;
 KW isotope; protease.

XX Synthetic.

XX W02003001206-A1.

XX 03-JAN-2003.

XX 25-JUN-2002; 2002WO-GB002921.

XX 26-JUN-2001; 2001GB-00015581.

XX (GLAX) GLAXO GROUP LTD.

XX Mckeown SC;

XX WPT; 2003-184066/18.

XX Analyzing cleavage of polymer, by providing polymer sample, incubating
 the sample with labeled isotope for cleavage at potential cleavage site,
 PT and analyzing the masses of any uncleaved fragments by mass spectrometry.

XX Example 3; Page 27; 73pp; English.

XX The present invention describes a method (M1) for analysing cleavage of a
 polymer. M1 comprises: (a) providing a sample of the polymer, a portion
 of the polymer molecules having been labeled at a position on one side of
 the potential cleavage site with a first isotopic label and a portion of
 the polymer molecules having been labeled at a position on the opposite
 side of the potential cleavage site with a second isotopic label; (b)
 incubating the sample under conditions suitable for cleavage at the
 potential cleavage site; and (c) analysing the mass(es) of any cleaved
 fragments by mass spectrometry and thereby determining whether and/or
 where cleavage has taken place. M1 is useful for analysing cleavage of a
 polymer, where the polymer is a linear polymer, and comprises a peptide
 or protein. Methods from the present invention can be used in discovering
 new or improved synthetic substrates for both known and unknown enzymes,
 e.g. enzymes identified from the human genome. The methods are also
 useful to identify the sequence origin, and in screening methods to
 identify new substrates for enzymes, in positional peptide scanning
 libraries, in *in vivo/ex vivo* peptide sequencing, and in assaying methods
 for oligonucleotide or peptide sequencing and in measuring differential
 protein expression. The methods are useful for monitoring the cleavage of
 polypeptides or polynucleotides, and for determining optimal polymer
 substrates. ABP57505 to ABP57605 represent peptides used in the
 exemplification of the present invention

SQ Sequence 5 AA;

Query Match 100.0%; Score 27; DB 6; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GDEVD 5
 |||||
 Db 1 GDEVD 5

RESULT 3

ABU63411
 ID ABU63411 standard; peptide; 5 AA.

XX

AC ABU63411;

XX 30-SEP-2003 (first entry)

XX Caspase-3 substrate peptide.

XX Caspase-3; colourimetric resonant reflectance optical biosensor; CROB;
 KW peak wavelength value; PWV; cell morphology; cell adhesion;
 KW cell migration; cell proliferation.

XX Synthetic.

XX Key Location/Qualifiers
 FH Modified-site 1
 FT /label= OTHER
 FT /note= "Gly is NHS-Gly"

FT Modified-site 5
 FT /label= OTHER
 FT /note= "Asp is covalently linked to a p-nitroanilide moiety"

XX US2003068657-A1.

XX 10-APR-2003.

XX 09-SEP-2002; 2002US-00237641.

XX 30-OCT-2000; 2000US-0244312P.

XX 12-APR-2001; 2001US-0283314P.

XX 03-JUL-2001; 2001US-0303028P.

XX 15-AUG-2001; 2001US-00930352.

XX 28-JAN-2002; 2002US-00058626.

XX 28-JAN-2002; 2002US-00059060.

XX 26-JUN-2002; 2002US-00180374.

XX 26-JUN-2002; 2002US-00180847.

XX 26-AUG-2002; 2002US-00227908.

XX (SRUB-) SRU BIOSYSTEMS LLC.

XX Lin B, Pepper J, Cunningham BT, Gerstenmaier J, Li P, Qiu J;

XX Plen H;

XX WPT; 2003-576423/54.

XX Detecting cleavage of one or more entire specific binding substances e.g.
 nucleic acids from surface of colorimetric resonant reflectance optical
 biosensor, by detecting peak wavelength value on biosensor's surface.

XX Example 7; Page 18; 65pp; English.

XX The invention detecting cleavage of entire specific binding substances
 from surface of a colourimetric resonant reflectance optical biosensor
 (CROB), where specific binding substances are immobilised on the surface
 of the biosensor at distinct locations, comprising detecting CROB peak
 wavelength value (PWV) of the distinct locations, applying cleaving
 molecule(s) to the locations, detecting a CROB PWV of the locations, and
 comparing the PWVs. Also included are detecting inhibition activity of
 one or more molecules against enzyme or binding partners that effect or
 bind molecules which cleave specific binding substances (which are
 immobilised on a surface of a CROB), detecting a change in a cell growth
 pattern (by growing cells on CROB), detecting a colourimetric resonant
 reflectance optical PWV, applying a test reagent to the cells, detecting

CC the colourimetric resonant reflectance optical PMW and discerning a
 CC difference between the colourimetric resonant reflectance optical PMW
 CC before and after application of the test reagent thereby indicating a
 CC change in a cell growth pattern and detecting the binding of molecules
 CC released from cells grown in a semi-permeable internal sleeve held in
 CC contact with CROB. The method of the invention is useful for detecting
 CC cleavage of one or more entire specific binding substances from a surface
 CC of a CROB. The specific binding substance is selected from nucleic acids,
 CC peptides, protein solutions, peptide solutions, single or double stranded
 CC DNA solutions, RNA solutions, RNA-DNA hybrid solutions, solutions
 CC containing compounds from a combinatorial chemical library, antigen,
 CC polyclonal antibody, monoclonal antibody, single chain antibody (scFv),
 CC Fab fragment, Fab'-2 fragment, Fv fragment, small organic molecule, a
 CC cell, virus, bacterial, polymer and biological samples. The other methods
 CC are useful for: (a) detecting inhibition activity of one or more
 CC molecules against enzyme or binding partners that effect or bind
 CC change in a cell growth pattern, such as cell morphology, cell adhesion,
 CC cell migration, cell proliferation and cell death; and detecting binding
 CC of molecules released from cells grown in a semi-permeable internal
 CC sleeve held in contact with CROB. The present sequence is a caspase-3
 CC substrate peptide used to demonstrate the biosensor's ability to detect
 CC cleaved small molecules
 XX

SQ Sequence 5 AA;

Query Match 100.0%; Score 27; DB 6; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
 |||||
 Db 1 GDEVD 5

RESULT 4
 AAY54043
 ID AAY54043 standard; peptide; 6 AA.

AC AAY54043;

DT 27-MAR-2000 (first entry)

XX Peptide sequence of the caspase-3 site.

XX Enhanced yellow mutant green fluorescent protein; EVFP; caspase-3;
 KW bioluminescence resonance energy transfer system; BRET system;
 KW bioluminescence protein; fluorophore; protein interaction;
 KW drug discovery; drug screening; gene function; toxicology; genotoxicity;
 KW Renilla luciferase.

OS Synthetic.

XX WO9966324-A2.

XX 23-DEC-1999.

XX 16-JUN-1999; 99WO-CA000561.

XX 16-JUN-1998; 98US-0089623P.

XX (JOLY/) JOLY E.
 PA (JOHN/) JOHNSON C H.
 PA (PIST/) PISTON D W.

XX Joly E, Johnson CH, Piston DW;

XX WPI; 2000-106136/09.

XX Novel energy transfer systems, used for assaying protein interactions,
 PT enzyme activities and the concentration of analytes or signaling
 PT molecules.

XX

PS Example 12; Page 55; 142pp; English.

XX The present sequence represents the caspase-3 site, which upon induction
 CC of apoptosis, should recognise and cleave the linker region of a fusion
 CC protein of Renilla luciferase (RLUC) and enhanced yellow mutant green
 CC fluorescent protein (EYFP). This separates RLUC and thereby decreases
 CC the BRET ratio over time. The fusion protein of RLUC and EYFP exemplifies
 CC the system of the invention. The specification describes a
 CC bioluminescence resonance energy transfer (BRET) system which comprises a
 CC bioluminescence protein (BP) that has luciferase activity, an acceptor
 CC fluorophore that can accept the energy from the BP when associated, in
 CC the presence of the substrate, a modulator that influences the proximity
 CC or orientation of the BP and the fluorophore, and a substrate to activate
 CC the luciferase activity of BP. The BRET system allows the detection of
 CC protein interactions without requiring exciting illumination. The BRET
 CC systems can be used for screening for second messengers and analytes.
 CC They can also be used for drug discovery, drug screening, to detect
 CC changes in protein-protein interaction, in functional genomics to
 CC determine the cellular function of a gene by determining its binding
 CC partner, in toxicology to measure the presence and concentration of toxic
 CC compounds, in diagnosis and in genotoxicity to measure the effect of a
 CC toxic compound on genome stability. In particular, it is useful for
 CC assaying protein interactions, enzyme activities and the concentration of
 CC analytes or signaling molecules in cells or in solution
 XX

SQ Sequence 6 AA;

Query Match 100.0%; Score 27; DB 3; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
 |||||
 Db 1 GDEVD 5

RESULT 5
 ABP57512
 ID ABP57512 standard; peptide; 6 AA.

AC ABP57512;

XX 28-APR-2003 (first entry)

XX Differentially isotopically labelled (DiMas) peptide #5.

XX Mass spectrometry; polymer; analysis; cleavage; substrate specificity;
 KW isotope; protease.

XX Synthetic.

XX WO2003001206-A1.

XX 03-JAN-2003.

XX 25-JUN-2002; 2002WO-GB002921.

XX 26-JUN-2001; 2001GB-00015581.

XX (GLAX) GLAXO GROUP LTD.

XX Mckeown SC;

XX WPI; 2003-184066/18.

XX Analyzing cleavage of polymer, by providing polymer sample, incubating
 PT the sample with labeled isotope for cleavage at potential cleavage site,
 PT and analyzing the masses of any uncleaved fragments by mass spectrometry.

PS Example 3; Page 22; 73pp; English.

XX The present invention describes a method (M1) for analysing cleavage of a
 CC polymer. M1 comprises: (a) providing a sample of the polymer, a portion

CC of the polymer molecules having been labeled at a position on one side of
 CC the potential cleavage site with a first isotopic label and a portion of
 CC the polymer molecules having been labeled at a position on the opposite
 CC side of the potential cleavage site with a second isotopic label; (b)
 CC incubating the sample under conditions suitable for cleavage at the
 CC potential cleavage site; and (c) analysing the mass(es) of any cleaved
 CC fragments by mass spectrometry and thereby determining whether and/or
 CC where cleavage has taken place. M1 is useful for analysing cleavage of a
 CC polymer, where the polymer is a linear polymer, and comprises a peptide
 CC or protein. Methods from the present invention can be used in discovering
 CC new or improved synthetic substrates for both known and unknown enzymes,
 CC e.g. enzymes identified from the human genome. The methods are also
 CC useful to identify the sequence origin, and in screening methods to
 CC identify new substrates for enzymes, in positional peptide scanning
 CC libraries, in *in vivo/ex vivo* peptide, and in assaying methods
 CC for oligonucleotide or peptide sequencing and in measuring differential
 CC protein expression. The methods are useful for monitoring the cleavage of
 CC polypeptides or polynucleotides, and for determining optimal polymer
 CC substrates. ABP57505 to ABP57605 represent peptides used in the
 CC exemplification of the present invention

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 27; DB 6; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
 DB 1 GDEVD 5

RESULT 6

AAW51893
 ID AAW51893 standard; peptide; 7 AA.

AC AAW51893;

DT 21-SEP-1998 (first entry)

XX Peptide useful for diagnosing diseases that involve apoptosis.

DE Immunogen; apoptosis; screen; inhibitor; stimulator; antibody; PARP;
 KW poly-ADP-ribose polymerase; antibody.

XX Mammalia.

OS WO9821590-A1.

XX 22-MAY-1998.

XX 13-NOV-1997; 97WO-US020214.

XX 15-NOV-1996; 96US-0030961P.

PR 12-NOV-1997; 97US-00967625.

XX (CEPH-) CEPHALON INC.

XX Siman R, Bozyczko-coyne D, Meyer SL, Bhat RV;

XX WPI; 1998-298113/26.

XX Peptide(s) containing epitope(s) characteristic of peptide(s) formed
 PT during apoptosis - useful for diagnosing diseases that involve apoptosis
 PT and to screen for inhibitors or stimulators of apoptosis.

XX Claim 1; Page 14; 40pp; English.

XX The invention relates to peptides that contain the sequences AAW51892-3.
 CC Also claimed are: (1) antibodies that bind specifically to an epitope on
 CC a peptide produced by apoptotic cells; (2) a method for identifying
 CC inhibitors or stimulators of apoptosis by measuring the effect of a test
 CC compound on amount of antibody bound to cell or tissue, and (3) kits for

CC detecting peptides produced by apoptotic cells. Antibodies are used in
 CC immunoassays to detect and quantify apoptosis, particularly for diagnosis
 CC of apoptosis-associated conditions, e.g. chronic neurodegeneration,
 CC cancer, sepsis, trauma to head or spine, hypoxia, anoxia, ischaemia,
 CC lesions and exposure to toxins, or susceptibility to such a condition
 XX SQ Sequence 7 AA;

Query Match 100.0%; Score 27; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDEVD 5
 DB 3 GDEVD 7

RESULT 7

AAO18998
 ID AAO18998 standard; peptide; 7 AA.

XX AAO18998;

DT 07-NOV-2002 (first entry)

XX Caspase-3 specific substrate peptide.

XX Enzymatic cleavage detection; linkage reaction detection; molar mass;
 KW molecular weight; pharmaceutical screening; contamination.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1. 7
 FT /note= "optionally modified to form maleimide-peptide 1-5
 FT -TAMRA or DNA-maleimide-peptidel-5-TAMRA"

FT Modified-site 1
 FT /note= "optionally modified by Fmoc"

FT Modified-site 2
 FT /note= "optionally modified by OtBu"

FT Modified-site 3
 FT /note= "optionally modified by OtBu"

FT Modified-site 5
 FT /note= "optionally modified by OtBu"

FT Modified-site 7
 FT /note= "optionally modified by (Mtt)-Harz"

XX WO200259352-A2.

XX 01-AUG-2002.

XX 28-JAN-2002; 2002WO-EP000845.

XX 26-JAN-2001; 2001EP-00101869.

XX (EVOT-) EVOTEC OAI AG.

XX Lopez-Calle E, Fries J, Jungmann J;

XX WPI; 2002-566851/60.

XX Detecting enzymatic cleavage and coupling reactions, useful e.g. in
 PT screening for pharmaceutical enzyme inhibitors, based on modular
 PT substrates.

XX Example 1; Page 27; 68pp; German.

XX The present invention relates to the detection of enzyme-catalysed
 CC cleavage reactions, comprising preparing a modular compound, including a
 CC reporter module Y, as substrate, incubating this with enzyme to produce
 CC at least two cleavage products, and determining enzyme activity by
 CC detecting the Y-containing products by a method that is sensitive to
 CC molecular weight. The method is used for testing specificity and activity

CC of enzymes or their modulators, identifying modulators and/or substrates,
 CC screening for pharmaceuticals (e.g. caspase inhibitors), diagnosis, and
 CC determining contamination in chemical or biological samples. The present
 CC sequence is a peptide substrate used in the exemplification of the
 CC invention
 XX
 SQ Sequence 7 AA;

Query Match 100.0%; Score 27; DB 5; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDEVD 5
 |||||
 Db 1 GDEVD 5

RESULT 8

AAW82031
 ID AAW82031 standard; peptide; 8 AA.

XX
 AC AAW82031;

XX
 DT 18-FEB-1999 (first entry)

XX Fluorogenic protease indicator protease binding peptide #9.

XX Protease activity; fluorophore; detection; fluorogenic; cellular uptake;
 KW conformation change.

XX Synthetic.

XX WO9837226-A1.

XX 27-AUG-1998.

XX 20-FEB-1998; 98WO-US003000.

XX 20-FEB-1997; 97US-00802981.

XX (ONCO-) ONCOIMMUNIN INC.

XX Komoriya A, Packard BS;

XX WPI; 1998-467579/40.

XX New fluorogenic compositions - containing 2 fluorophores separated by a
 PT peptide comprising a protease binding site, used for detecting protease
 PT activity in samples.

XX Claim 2; Page 77; 90pp; English.

XX AAW82023-W82240 are peptides used in the construction of a fluorogenic
 CC composition which is used for the detection of protease activity in
 CC biological samples. The products can be used for the detection of
 CC conformation changes in nucleic acids, oligosaccharides, polysaccharides,
 CC proteins, peptides, lipids, phospholipids, glycolipids, glycoproteins,
 CC steroids or polymers. In addition, attachment of a hydrophobic group to a
 CC molecule can be used to enhance uptake by cells. The composition is
 CC composed of P = peptide comprising a protease binding site for the
 CC protease, F1, F2 peptides = fluorophores where F1 is attached to the
 CC amino terminal amino acid and F2 is attached to the carboxyl terminal
 CC amino acid and S1, S2 peptides = when present, are peptide spacers where
 CC S1, when present, is attached to the amino terminal acid, and S2, when
 CC present, is attached to the carboxyl terminal amino acid

XX Sequence 8 AA;

Query Match 100.0%; Score 27; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDEVD 5

Db |||||
 1 GDEVD 5

RESULT 9

AAW82030
 ID AAW82030 standard; peptide; 8 AA.

XX AAW82030;

XX 18-FEB-1999 (first entry)

XX Fluorogenic protease indicator protease binding peptide #8.

XX Protease activity; fluorophore; detection; fluorogenic; cellular uptake;
 KW conformation change.

XX Synthetic.

XX WO9837226-A1.

XX 27-AUG-1998.

XX 20-FEB-1998; 98WO-US003000.

XX 20-FEB-1997; 97US-00802981.

XX (ONCO-) ONCOIMMUNIN INC.

XX Komoriya A, Packard BS;

XX WPI; 1998-467579/40.

XX New fluorogenic compositions - containing 2 fluorophores separated by a
 PT peptide comprising a protease binding site, used for detecting protease
 PT activity in samples.

XX Claim 2; Page 77; 90pp; English.

XX AAW82023-W82240 are peptides used in the construction of a fluorogenic
 CC composition which is used for the detection of protease activity in
 CC biological samples. The products can be used for the detection of
 CC conformation changes in nucleic acids, oligosaccharides, polysaccharides,
 CC proteins, peptides, lipids, phospholipids, glycolipids, glycoproteins,
 CC steroids or polymers. In addition, attachment of a hydrophobic group to a
 CC molecule can be used to enhance uptake by cells. The composition is
 CC composed of P = peptide comprising a protease binding site for the
 CC protease, F1, F2 peptides = fluorophores where F1 is attached to the
 CC amino terminal amino acid and F2 is attached to the carboxyl terminal
 CC amino acid and S1, S2 peptides = when present, are peptide spacers where
 CC S1, when present, is attached to the amino terminal acid, and S2, when
 CC present, is attached to the carboxyl terminal amino acid

XX Sequence 8 AA;

Query Match 100.0%; Score 27; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDEVD 5
 |||||
 Db 1 GDEVD 5

RESULT 10

AAG73266
 ID AAG73266 standard; peptide; 8 AA.

XX AAG73266;

XX 14-AUG-2001 (first entry)

XX Protease indicator peptide #21.

XX Protease detection; peptide cleavage; enzyme activity; fluorogenic;
 KW viral infection; cancer metastasis; emphysema; arthritis; thrombosis;
 KW haemophilia.
 XX Synthetic.
 XX WO200118238-A1.
 XX 15-MAR-2001.
 XX 11-SEP-2000; 2000WO-US024882.
 XX 10-SEP-1999; 99US-00394019.
 XX (ONCO-) ONCOIMMUNIN INC.
 XX Komoriya A, Packard BS;
 XX WPI; 2001-389573/41.
 XX New fluorogenic compositions whose fluorescence level increases in the
 PT presence of active proteases, useful for detecting and localizing
 PT protease activity in biological samples, particularly in frozen tissue
 PT samples.
 XX Example 14; Page 65; 86pp; English.
 XX The present invention describes fluorogenic compositions which can be
 CC used for the detection of protease activity. This can be useful as an
 CC indicator of viral infection, cancer metastasis, haemophilia, emphysema,
 CC thrombosis and arthritis. The fluorogenic compositions comprise a
 CC peptide, a peptide spacer and a donor and an acceptor fluorophore. The
 CC peptide is cleaved by a protease and the fluorophores can then be
 CC detected. The present sequence is one of the peptides described in the
 CC exemplification of the invention
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 27; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GDEVD 5
 |||||
 Db 1 GDEVD 5
 RESULT 11
 ABU60376
 ID ABU60376 standard; peptide; 8 AA.
 XX
 AC ABU60376;
 XX
 DT 29-APR-2003 (first entry)
 XX
 DE Protease binding peptide motif SEQ ID 34.
 XX
 KW Protease; indicator; chromophore; H-dimer; fluorescence; absorbance;
 KW nuclease; screening; fluorophore; substrate cleavage.
 XX
 OS Synthetic.
 XX
 FN WO200261038-A2.
 XX
 PD 08-AUG-2002.
 XX
 PD 21-DEC-2001; 2001WO-US049781.
 XX
 PF 22-DEC-2000; 2000US-00747287.
 XX
 PR (ONCO-) ONCOIMMUNIN INC.
 XX
 PA

PI Packard BS, Komoriya A;
 XX WPI; 2002-698548/75.
 XX
 PT Indicator composition comprising polypeptide or nucleic acid backbone
 PT joining two same chromophores resulting in quenching of fluorescence
 PT of/change in absorbance of chromophores, useful for detecting protease
 PT activity.
 XX
 PS Disclosure; Page 30; 97pp; English.
 XX
 CC This invention describes a novel indicator composition (referred as homo-
 CC doubly labeled compositions) comprising a polypeptide backbone or a
 CC nucleic acid backbone joining two chromophores of the same species
 CC whereby the chromophores form an H-dimer resulting in quenching of the
 CC fluorescence of or a change in the absorbance of the chromophore, a
 CC decrease in fluorescence or a change in absorbance indicates that the
 CC first molecule and the second molecule are interacting. The indicator is
 CC useful for detecting the activity of a protease, where an increase in
 CC fluorescence or a change in absorbance indicates that the protease
 CC cleaves the polypeptide backbone. The indicator is attached to a solid
 CC support inside a mammalian, yeast or insect cell. The composition bears a
 CC hydrophobic group such as Fmoc, 9-fluorenylmethyl group, 1-
 CC fluorenylmethyl group, 9-fluorenylmethyl group, and 9-fluorenylmethyl-1-
 CC carboxylic group, benzoyloxycarbonyl, Xanthyl (Xan), Trityl (Trt), 4-
 CC methyltrityl (Mtt), 4-methoxytrityl (Mmt), 4-methoxy-2,3,6-trimethyl-
 CC benzenesulphonyl (Mtr), Mesitylene-2-sulphonyl (Mts), 4,4'-
 CC dimethoxybenzhydryl (Mbh), etc. The method described in the invention is
 CC useful for detecting protease or nuclease activity (or the presence of
 CC nucleic acid) in histological section, cells in culture, (e.g., seeded or
 CC cultured adherent cells), a biological sample such as tissue, biopsy,
 CC lymph, embryo, or whole animal, or cell suspension derived from a
 CC biological sample such as tissue, blood, urine, saliva, lymph, or biopsy.
 CC The indicator composition is also useful for screening a test agent for
 CC the ability to modulate a protease (or a nuclease, lipase, etc.). The
 CC indicator reagents allow rapid determination of protease activity in a
 CC matter of minutes in a single-step procedure. The fluorescent indicators
 CC both absorb and emit in the visible range (400-800 nm). These signals are
 CC therefore not readily quenched by, nor is activation of the fluorophores,
 CC that is, absorption of light, interfered with by background molecules;
 CC therefore they are easily detected in biological samples. The fluorogenic
 CC protease indicators utilise high efficiency fluorophores and are able to
 CC achieve a high degree of quenching while providing a strong signal when
 CC the quench is released by cleavage of the peptide substrate. The high
 CC signal allows detection of very low levels of protease activity. Thus the
 CC fluorogenic protease indicators are particularly well suited for in situ
 CC detection of protease activity. ABU60357-ABU60477 represent peptides use
 CC to illustrate the method described in the disclosure of the invention
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 27; DB 5; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GDEVD 5
 |||||
 Db 1 GDEVD 5
 RESULT 12
 ABU60473
 ID ABU60473 standard; peptide; 8 AA.
 XX
 AC ABU60473;
 XX
 DT 29-APR-2003 (first entry)
 XX
 DE Central protease recognition domain SEQ ID 206.
 XX
 KW Protease; indicator; chromophore; H-dimer; fluorescence; absorbance;
 KW nuclease; screening; fluorophore; substrate cleavage.
 XX

OS Synthetic.
 PN WO200261038-A2.
 XX
 PD 08-AUG-2002.
 XX
 XX 21-DEC-2001; 2001WO-US049781.
 PF
 XX 22-DEC-2000; 2000US-00747287.
 PR
 XX (ONCO-) ONCOIMMUNIN INC.
 PA
 XX Packard BS, Komoriya A;
 XX WPI; 2002-698548/75.
 DR
 XX
 XX Indicator composition comprising polypeptide or nucleic acid backbone
 PT joining two same chromophores resulting in quenching of fluorescence
 PT of/change in absorbance of chromophores, useful for detecting protease
 PT activity.
 PT
 PS Example 14; Page 73; 97pp; English.
 XX
 XX This invention describes a novel indicator composition (referred as homo-
 CC doubly labeled compositions) comprising a polypeptide backbone or a
 CC nucleic acid backbone joining two chromophores of the same species
 CC whereby the chromophores form an H-dimer resulting in quenching of the
 CC fluorescence of or a change in the absorbance of the chromophore, a
 CC decrease in fluorescence or a change in absorbance indicates that the
 CC first molecule and the second molecule are interacting. The indicator is
 CC useful for detecting the activity of a protease, where an increase in
 CC fluorescence or a change in absorbance indicates that the protease
 CC cleaves the polypeptide backbone. The indicator is attached to a solid
 CC support inside a mammalian, yeast or insect cell. The composition bears a
 CC hydrophobic group such as Fmoc, 9-fluoreneacetyl group, 1-
 CC fluorinecarboxylic group, 9-fluoreneacetyl group, and 9-fluorenone-1-
 CC carboxylic group, benzoyloxycarbonyl, xanthyl (Xan), Trityl (Trt), 4-
 CC methyltrityl (Mtt), 4-methoxytrityl (Mmt), 4-methoxy-2,3, 6-trimethyl-
 CC benzenesulphonyl (Mtr), Mesitylene-2-sulphonyl (Mts), 4,4'-
 CC dimethoxybenzhydryl (Mbh), etc. The method described in the invention is
 CC useful for detecting protease or nuclease activity (or the presence of
 CC nucleic acid) in histological section, cells in culture, (e.g., seeded or
 CC cultured adherent cells), a biological sample such as tissue, biopsy,
 CC lymph, embryo, or whole animal, or cell suspension derived from a
 CC biological sample such as tissue, blood, urine, saliva, lymph, or biopsy.
 CC The indicator composition is also useful for screening a test agent for
 CC the ability to modulate a protease (or a nuclease, lipase, etc.). The
 CC indicator reagents allow rapid determination of protease activity in a
 CC matter of minutes in a single-step procedure. The fluorescent indicators
 CC both absorb and emit in the visible range (400-800 nm). These signals are
 CC therefore not readily quenched by, nor is activation of the fluorophores,
 CC that is, absorption of light, interfered with by background molecules;
 CC therefore they are easily detected in biological samples. The fluorogenic
 CC protease indicators utilize high efficiency fluorophores and are able to
 CC achieve a high degree of quenching while providing a strong signal when
 CC the quench is released by cleavage of the peptide substrate. The high
 CC signal allows detection of very low levels of protease activity. Thus the
 CC fluorogenic protease indicators are particularly well suited for in situ
 CC detection of protease activity. ABU60357-ABU60477 represent peptides use
 CC to illustrate the method described in the disclosure of the invention
 XX

SQ Sequence 8 AA;
 Query Match 100.0%; Score 27; DB 5; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GDEVD 5
 |
 |
 |
 |
 |
 DB 1 GDEVD 5
 RESULT 13

ABU60370
 ID ABU60370 standard; peptide; 8 AA.
 XX
 AC ABU60370;
 XX
 DT 29-APR-2003 (first entry)
 XX
 DE Protease binding peptide motif SEQ ID 14.
 XX
 XX Protease; indicator; chromophore; H-dimer; fluorescence; absorbance;
 KW nuclease; screening; fluorophore; substrate cleavage.
 XX
 XX Synthetic.
 OS
 XX WO200261038-A2.
 PN
 XX
 XX 08-AUG-2002.
 PD
 XX 21-DEC-2001; 2001WO-US049781.
 PF
 XX 22-DEC-2000; 2000US-00747287.
 PR
 XX (ONCO-) ONCOIMMUNIN INC.
 PA
 XX Packard BS, Komoriya A;
 XX WPI; 2002-698548/75.
 DR
 XX Indicator composition comprising polypeptide or nucleic acid backbone
 PT joining two same chromophores resulting in quenching of fluorescence
 PT of/change in absorbance of chromophores, useful for detecting protease
 PT activity.
 PT
 PS Disclosure; Page 29; 97pp; English.
 XX
 XX This invention describes a novel indicator composition (referred as homo-
 CC doubly labeled compositions) comprising a polypeptide backbone or a
 CC nucleic acid backbone joining two chromophores of the same species
 CC whereby the chromophores form an H-dimer resulting in quenching of the
 CC fluorescence of or a change in the absorbance of the chromophore, a
 CC decrease in fluorescence or a change in absorbance indicates that the
 CC first molecule and the second molecule are interacting. The indicator is
 CC useful for detecting the activity of a protease, where an increase in
 CC fluorescence or a change in absorbance indicates that the protease
 CC cleaves the polypeptide backbone. The indicator is attached to a solid
 CC support inside a mammalian, yeast or insect cell. The composition bears a
 CC hydrophobic group such as Fmoc, 9-fluoreneacetyl group, 1-
 CC fluorinecarboxylic group, 9-fluoreneacetyl group, and 9-fluorenone-1-
 CC carboxylic group, benzoyloxycarbonyl, xanthyl (Xan), Trityl (Trt), 4-
 CC methyltrityl (Mtt), 4-methoxytrityl (Mmt), 4-methoxy-2,3, 6-trimethyl-
 CC benzenesulphonyl (Mtr), Mesitylene-2-sulphonyl (Mts), 4,4'-
 CC dimethoxybenzhydryl (Mbh), etc. The method described in the invention is
 CC useful for detecting protease or nuclease activity (or the presence of
 CC nucleic acid) in histological section, cells in culture, (e.g., seeded or
 CC cultured adherent cells), a biological sample such as tissue, biopsy,
 CC lymph, embryo, or whole animal, or cell suspension derived from a
 CC biological sample such as tissue, blood, urine, saliva, lymph, or biopsy.
 CC The indicator composition is also useful for screening a test agent for
 CC the ability to modulate a protease (or a nuclease, lipase, etc.). The
 CC indicator reagents allow rapid determination of protease activity in a
 CC matter of minutes in a single-step procedure. The fluorescent indicators
 CC both absorb and emit in the visible range (400-800 nm). These signals are
 CC therefore not readily quenched by, nor is activation of the fluorophores,
 CC that is, absorption of light, interfered with by background molecules;
 CC therefore they are easily detected in biological samples. The fluorogenic
 CC protease indicators utilize high efficiency fluorophores and are able to
 CC achieve a high degree of quenching while providing a strong signal when
 CC the quench is released by cleavage of the peptide substrate. The high
 CC signal allows detection of very low levels of protease activity. Thus the
 CC fluorogenic protease indicators are particularly well suited for in situ
 CC detection of protease activity. ABU60357-ABU60477 represent peptides use
 CC to illustrate the method described in the disclosure of the invention
 XX

